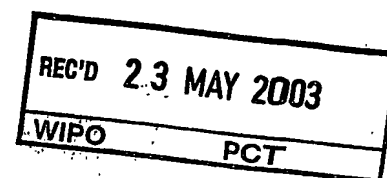


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Maiken Lind



10 APR. 2002

TITLE: Improved *Bacillus* Host Cell

Modtaget

TECHNICAL FIELD

Bacillus sp. are attractive hosts for the production of heterologous proteins due their ability to secrete proteins directly into the culture medium. They have a high capacity for protein secretion, are genetically highly amenable, nonpathogenic and free of endotoxins, and consequently a large variety of proteins from different organisms have been efficiently produced and secreted in *Bacillus* sp. i.e. in *Bacillus licheniformis*.

Improved *Bacillus* host cells that provide better production economy, or better products e.g. in terms of stability, purity etc. are constantly in demand in the industry.

BACKGROUND

Industrial production in *Bacillus* sp. of products of interest such as heterologous polypeptides, amino acids, carbohydrates etc., even when such a product is secreted into the medium, very often requires a costly purification step of the product from the culture medium. Contaminant polypeptides native to the *Bacillus* production host cell are secreted into the culture medium, and they may have to be removed e.g. in order to ensure the stability of the product, or to obtain a sufficient purity of the product. Typically, the native secreted contaminant polypeptides could be proteolytic enzymes, nutrient uptake factors, signal molecules etc.

Naturally, it is of considerable interest to the industrial producers to reduce the costs associated with product purification steps, indeed it would be of commercial value if one or more purification steps could be completely eliminated.

SUMMARY

A problem to be solved by the present invention is how to reduce the necessary product purification required when producing products of interest in a *Bacillus licheniformis* host cell. The present invention provides a solution to the problem by reducing the amount of contaminant secreted native polypeptide(s) in the culture medium, this is achieved by reducing the expression of such polypeptide(s) in a mutated host cell. Production in a mutant host cell of the invention provides a culture medium with far fewer contaminants, and this in turn makes it much easier to purify the product of interest from the culture medium to the point where certain previously required steps may be completely eliminated from the production process. Production in a mutant host cell of the invention may also have a positive effect on the total product yield and shelf-life, since product stability is often hampered by the presence of contaminant polypeptides in the culture medium.

Accordingly, in a first aspect the invention relates to a *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more secreted polypeptide(s) which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 200, preferably at least 85% identical, more preferably at least 90% identical, still more preferably at least 95% identical, and most preferably at least 97% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 200, wherein the mutant host cell secretes at least 5% less of the one or more secreted polypeptide(s) than the parent host cell, when they are cultivated under comparable conditions.

Preferably wherein the mutant host cell secretes at least 10% less, more preferably at least 20% less, still more preferably at least 30% less, even more preferably at least 40% less, yet more preferably at least 50% less, or at least 60% less, or at least 70% less, or at least 80%, or most preferably at least 90% less of the one or more secreted polypeptide(s) than the parent host cell, when they are cultivated under comparable conditions. Most preferably the mutant host cell secretes absolutely nothing of the one or more secreted polypeptide(s).

Comparable conditions of cultivation must be used in order to compare the secretion level of one or more secreted polypeptides in a mutant host cell of the invention with that in a parent host cell. They are cultivated separately under identical conditions in identical setups, of course allowing for the usual standard deviations of the operating parameters normally associated with growth experiments, such as temperature control etc. The quantification of the expression level of one or more secreted polypeptide(s) is done by standard text-book assay techniques as known in the art, often based on the biological activity of the one or more secreted polypeptide(s) *i.e.* if a secreted polypeptide is an amylase, then an amylase-activity based quantification assay is used. To quantify a secreted polypeptide of unknown activity, immuno based or mass-spec based assays may be used.

In a second aspect the invention relates to a process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in the previous aspect in a suitable medium, whereby the said product is produced.

Finally, an aspect of the invention relates to a use of a *Bacillus licheniformis* mutant host cell as defined in the first aspect for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced.

DEFINITIONS

Nucleic acid construct: When used herein, the term "nucleic acid construct" means a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring gene or which has been modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature. The term nucleic acid construct is synonymous with the term "expression cassette" when the nucleic acid construct contains the control sequences required for expression of a coding sequence of the present invention.

Control sequence: The term "control sequences" is defined herein to include all components, which are necessary or advantageous for the expression of a polypeptide of the present invention. Each control sequence may be native or foreign to the nucleotide sequence encoding the polypeptide. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the nucleotide sequence encoding a polypeptide.

Operably linked: The term "operably linked" is defined herein as a configuration in which a control sequence is appropriately placed at a position relative to the coding sequence of the DNA sequence such that the control sequence directs the expression of a polypeptide.

Coding sequence: When used herein the term "coding sequence" is intended to cover a nucleotide sequence, which directly specifies the amino acid sequence of its protein product. The boundaries of the coding sequence are generally determined by an open reading frame, which usually begins with the ATG start codon. The coding sequence typically include DNA, cDNA, and recombinant nucleotide sequences.

Expression: In the present context, the term "expression" includes any step involved in the production of the polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

Expression vector: In the present context, the term "expression vector" covers a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of the invention, and which is operably linked to additional segments that provide for its transcription.

DETAILED DISCLOSURE

A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more secreted polypeptide(s) which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 200, wherein the mutant host cell secretes at least 5% less of the one or more secreted polypeptide(s) than the parent host cell, when they are cultivated under comparable conditions.

The term "parent host cell" in the context of the present invention means a cell which is genetically identical, or isogenic, to the progeny mutant or mutant cell of the present invention, except for the mutated one or more gene(s) encoding one or more secreted polypeptide(s) in said mutant.

The degree of identity, or %-identity of polypeptide sequences can suitably be investigated by aligning the sequences using a computer program known in the art, such as "GAP" provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711)(Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-453). Using GAP with the following settings for DNA sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3".

The object of the present invention is to provide a cleaner culture medium so as to reduce the product purification to a minimum, and this may be done according to the invention by reducing or even completely abolishing the expression of genes expressing native secreted polypeptides via mutagenisation of those genes. One of the very well-known method of ensuring that a gene is not expressed into an active polypeptide within a cell is simply to delete or partially delete the encoding gene. Many techniques have been described in the art on how to specifically delete or partially delete one or more gene(s) in the genome of a cell, and certainly from the genome of a *Bacillus licheniformis* cell (see e.g. Novozymes A/S WO 01/90393, Novozymes A/S WO 02/00907, and Example 1 herein). Accordingly, a preferred embodiment of the present invention relates to a host cell of the first aspect, which is mutated by a partial or complete deletion of the one or more gene(s) encoding the one or more secreted polypeptide(s).

A specific example of such a deletion or partial deletion is shown in an example herein, where a gene encoding the native secreted polypeptide shown in SEQ ID NO: 134 is deleted from a *Bacillus licheniformis* host cell. So, a preferred embodiment of the present invention

relates to a host cell of the first aspect, which is mutated by a partial or complete deletion of a gene encoding a secreted polypeptide which is at least 80% identical to the polypeptide shown in SEQ ID NO: 134, more preferably at least 85%, still more preferably at least 90%, even more preferably at least 95%, and most preferably at least 97% identical to the polypeptide shown in SEQ ID NO: 134.

As already mentioned, it is an object of the invention to provide a cleaner culture medium, and the more secreted contaminant polypeptides that are eliminated, the fewer will have to be removed in a subsequent product purification. A preferred embodiment of the present invention relates to a host cell of the first aspect, which is mutated in two or more genes encoding two or more secreted polypeptides.

The product of interest to be produced by the mutant host cell of the first aspect may be one or more polypeptide(s) encoded by one or more heterologous gene(s). Consequently, a preferred embodiment of the present invention relates to a host cell of the first aspect, which comprises one or more heterologous gene(s) encoding one or more heterologous polypeptide(s).

In the industrial production of polypeptides it is of interest to achieve a product yield as high as possible. One way to increase the yield is to increase the copy number of a gene encoding a polypeptide of interest. This can be done by placing the gene on a high copy number plasmid. However, plasmids are unstable and are often lost from the host cells if there is no selective pressure during the cultivation of the host cells. Another way to increase the copy number of the gene of interest is to integrate it into the host cell chromosome in multiple copies. Integration of two genes has been described in WO 91/09129 and WO 94/14968 (Novozymes A/S) the content of which is hereby incorporated by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) is present in at least two copies, preferably at least 4 copies, and most preferably at least 6 copies. In another embodiment the heterologous gene(s) is present in at least ten copies. If carried on a plasmid the gene(s) may be present in several hundred copies per cell, so in a still further embodiment of the present invention the heterologous gene(s) is present in at least 100 copies.

Integration of two genes closely spaced in anti-parallel tandem to achieve better stability has been described in WO 99/41358 (Novozymes A/S) the content of which is hereby incorporated by reference, as well as the stable chromosomal multi-copy integration of genes described in WO 02/00907 (Novozymes A/S) the content of which is incorporated herein by

reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are stably integrated into the genome of the cell.

5 Selection of chromosomal integrant has for convenience resulted in the use of selectable markers such as antibiotic resistance markers. However it is desirable if possible to avoid the use of antibiotic marker genes. WO 01/90393 discloses a method for the integration of a gene in the chromosome of a host cell without leaving antibiotic resistance markers behind in the strain, the content of which is hereby incorporated by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect wherein the heterologous
10 gene(s) is integrated into the genome of the cell without leaving any antibiotic resistance marker genes at the site of integration.

The present invention also relates to nucleic acid constructs comprising a nucleotide sequence encoding a product of interest, which may be operably linked to one or more
15 control sequences that direct the expression of the coding sequence in a suitable host cell under conditions compatible with the control sequences.

A nucleotide sequence encoding a polypeptide of interest may be manipulated in a variety of ways to provide for expression of the polypeptide. Manipulation of the nucleotide sequence prior to its insertion into a vector may be desirable or necessary depending on the expression
20 vector. The techniques for modifying nucleotide sequences utilizing recombinant DNA methods are well known in the art.

Other ways of increasing the product yield would be to increase promoter activity of the
25 specific promoter regulating the expression of a specific gene of interest. Also a more general increase in the activity of several promoters at the same time could lead to an improved product yield. The control sequence may be an appropriate promoter sequence, a nucleotide sequence which is recognized by a host cell for expression of the nucleotide sequence. The promoter sequence contains transcriptional control sequences, which
30 mediate the expression of the polypeptide. The promoter may be any nucleotide sequence which shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

35 Examples of suitable promoters for directing the transcription of the nucleic acid constructs of the present invention, especially in a bacterial host cell, are the promoters obtained from the *E. coli* lac operon, *Streptomyces coelicolor* agarase gene (*dagA*), *Bacillus subtilis*

levansucrase gene (sacB), *Bacillus licheniformis* alpha-amylase gene (amyL), *Bacillus stearothermophilus* maltogenic amylase gene (amyM), *Bacillus amyloliquefaciens* alpha-amylase gene (amyQ), *Bacillus licheniformis* penicillinase gene (penP), *Bacillus subtilis* xylA and xylB genes, and prokaryotic beta-lactamase gene (Villa-Kamaroff et al., 1978, 5 Proceedings of the National Academy of Sciences USA 75: 3727-3731), as well as the tac promoter (DeBoer et al., 1983, Proceedings of the National Academy of Sciences USA 80: 21-25). Further promoters are described in "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242: 74-94; and in Sambrook et al., 1989, supra.

10 Other useful promoters are described in WO 93/10249, WO 98/07846, and WO 99/43835 (Novozymes A/S) the contents of which are incorporated fully herein by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are transcribed from a heterologous promoter or from an artificial promoter.

15 The control sequence may also be a suitable transcription terminator sequence, a sequence recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3' terminus of the nucleotide sequence encoding the polypeptide. Any terminator which is functional in the host cell of choice may be used in the present invention.

20 The control sequence may also be a suitable leader sequence, a nontranslated region of an mRNA which is important for translation by the host cell. The leader sequence is operably linked to the 5' terminus of the nucleotide sequence encoding the polypeptide. Any leader sequence that is functional in the host cell of choice may be used in the present invention.

25 The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3' terminus of the nucleotide sequence and which, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence which is functional in the host cell of choice may be used in the 30 present invention.

The control sequence may also be a signal peptide coding region that codes for an amino acid sequence linked to the amino terminus of a polypeptide and directs the encoded polypeptide into the cell's secretory pathway. The 5' end of the coding sequence of the 35 nucleotide sequence may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted polypeptide. Alternatively, the 5' end of the coding sequence may contain a signal peptide

coding region which is foreign to the coding sequence. The foreign signal peptide coding region may be required where the coding sequence does not naturally contain a signal peptide coding region. Alternatively, the foreign signal peptide coding region may simply replace the natural signal peptide coding region in order to enhance secretion of the polypeptide. However, any signal peptide coding region which directs the expressed polypeptide into the secretory pathway of a host cell of choice may be used in the present invention.

Effective signal peptide coding regions for bacterial host cells are the signal peptide coding regions obtained from the genes for *Bacillus* NCIB 11837 maltogenic amylase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus licheniformis* subtilisin, *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* neutral proteases (nprT, nprS, nprM), and *Bacillus subtilis* prsA. Further signal peptides are described by Simonen and Palva, 1993, *Microbiological Reviews* 57: 109-137.

The control sequence may also be a propeptide coding region that codes for an amino acid sequence positioned at the amino terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to a mature active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding region may be obtained from the genes for *Bacillus subtilis* alkaline protease (aprE), *Bacillus subtilis* neutral protease (nprT), *Saccharomyces cerevisiae* alpha-factor, *Rhizomucor miehei* aspartic proteinase, and *Myceliophthora thermophila* laccase (WO 95/33836).

Where both signal peptide and propeptide regions are present at the amino terminus of a polypeptide, the propeptide region is positioned next to the amino terminus of a polypeptide and the signal peptide region is positioned next to the amino terminus of the propeptide region.

It may also be desirable to add regulatory sequences which allow the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those which cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory systems in prokaryotic systems include the lac, tac, and trp operator systems. In yeast, the ADH2 system or GAL1 system may be used. In eukaryotic systems, these include the dihydrofolate reductase gene which is amplified in the presence of methotrexate, and the

metallothionein genes which are amplified with heavy metals. In these cases, the nucleotide sequence encoding the polypeptide would be operably linked with the regulatory sequence.

5 The present invention also relates to recombinant expression vectors comprising the nucleic acid construct of the invention. The various nucleotide and control sequences described above may be joined together to produce a recombinant expression vector which may include one or more convenient restriction sites to allow for insertion or substitution of the nucleotide sequence encoding the polypeptide at such sites. Alternatively, the nucleotide sequence of the present invention may be expressed by inserting the nucleotide sequence or
10 a nucleic acid construct comprising the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

The recombinant expression vector may be any vector (e.g., a plasmid or virus) which can be
15 conveniently subjected to recombinant DNA procedures and can bring about the expression of the nucleotide sequence. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vectors may be linear or closed circular plasmids.

20 The vector may be an autonomously replicating vector, i.e., a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome.

25 The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host cell, or a transposon may be used.

30

The vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

35

Examples of bacterial selectable markers are the *dal* genes from *Bacillus subtilis* or *Bacillus licheniformis*, or markers which confer antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracycline resistance.

- 5 The vectors of the present invention preferably contain an element(s) that permits stable integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

10 For integration into the host cell genome, the vector may rely on the nucleotide sequence encoding the polypeptide or any other element of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination. Alternatively, the vector may contain additional nucleotide sequences for directing integration by homologous recombination into the genome of the host cell. The additional nucleotide sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the
15 chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should preferably contain a sufficient number of nucleotides, such as 100 to 1,500 base pairs, preferably 400 to 1,500 base pairs, and most preferably 800 to 1,500 base pairs, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be
20 any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding nucleotide sequences. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

- 25 For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, and pACYC184 permitting replication in *E. coli*, and pUB110, pE194, pTA1060, and pAM β 1 permitting replication in *Bacillus*. The origin of replication may be one having a mutation
30 which makes its functioning temperature-sensitive in the host cell (see, e.g., Ehrlich, 1978, Proceedings of the National Academy of Sciences USA 75: 1433).

35 More than one copy of a nucleotide sequence of the present invention may be inserted into the host cell to increase production of the gene product. An increase in the copy number of the nucleotide sequence can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the nucleotide sequence where cells containing amplified copies of the selectable

marker gene, and thereby additional copies of the nucleotide sequence, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

5 The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, e.g., Sambrook et al., 1989, supra).

10 The introduction of a vector into a bacterial host cell may, for instance, be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, Molecular General Genetics 168: 111-115), using competent cells (see, e.g., Young and Spizizin, 1961, Journal of Bacteriology 81: 823-829, or Dubnau and Davidoff-Abelson, 1971, Journal of Molecular Biology 56: 209-221), electroporation (see, e.g., Shigekawa and Dower, 1988, Biotechniques 6: 742-751), or conjugation (see, e.g., Koehler and Thorne, 1987, Journal of Bacteriology 169: 5771-5278).

15 A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are comprised in an operon, preferably a polycistronic operon. The term "operon" in the context of the present invention means a polynucleotide comprising several genes that are clustered and perhaps even transcribed together into a polycistronic mRNA, e.g. genes coding for the enzymes of a metabolic pathway. The transcription of an operon may be initiated at a promoter region and controlled by a neighboring regulatory gene, which encodes a regulatory protein, which in turn binds to the operator sequence in the operon to respectively inhibit or enhance the transcription. The gene or the operon can be carried on a suitable plasmid that can be stably maintained, e.g. 20 capable of stable autonomous replication in the host cell (the choice of plasmid will typically depend on the compatibility of the plasmid with the host cell into which the plasmid is to be introduced) or it can be carried on the chromosome of the host. The said gene may be endogenous to the host cell in which case the product of interest is a protein naturally produced by the host cell and in most cases the gene will be in its normal position on the chromosome. If the gene encoding the product of interest is an exogenous gene, the gene 30 could either be carried on a suitable plasmid or it could be integrated on the host chromosome. In one embodiment of the invention the eubacterium is a recombinant eubacterium. Also the product of interest may in another embodiment be a recombinant protein.

35 The product of interest is any gene product or product of a metabolic pathway which is industrially useful and which can be produced in a bacterial cell such as a *B. licheniformis*.

In one preferred embodiment, the heterologous polypeptide(s) is an antimicrobial peptide, or a fusion peptide comprising a peptide part which in its native form has antimicrobial activity.

- 5 In another preferred embodiment, the heterologous polypeptide(s) has biosynthetic activity and produces a compound or an intermediate of interest.

Yet another embodiment relates to a host cell of the first aspect, wherein the compound or intermediate of interest comprises vitamins, amino acids, antibiotics, carbohydrates, or
10 surfactants, and preferably the carbohydrates comprise hyaluronic acid.

In one embodiment the heterologous polypeptide(s) is an enzyme, particularly the enzyme is an enzyme of a class selected from the group of enzyme classes consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC 3), lyases (EC 4), isomerases
15 (EC 5), and ligases (EC 6). Preferably the enzyme is an enzyme with an activity selected from the group consisting of aminopeptidase, amylase, amyloglucosidase, mannanase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase,
20 isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, or xylanase. Preferably the enzyme is an amylase or a mannanase.

A second aspect of the invention relates to a process for producing at least one product of
25 interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in the first aspect of the invention in a suitable medium, whereby the said product is produced. One embodiment relates to a process of the second aspect, further comprising isolating or purifying the product of interest. Suitable media for the cultivation is described below as well as methods for the purification or isolation of the
30 produced product which is an optional additional step to the process of the present invention.

In the production methods of the present invention, the cells are cultivated in a nutrient medium suitable for production of the polypeptide using methods known in the art. For example, the cell may be cultivated by shake flask cultivation, small-scale or large-scale
35 fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors performed in a suitable medium and under conditions allowing the polypeptide to be expressed and/or isolated. The cultivation takes place in a

suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (e.g., in catalogues of the American Type Culture Collection). If the polypeptide is secreted into the nutrient medium, the polypeptide
5 can be recovered directly from the medium. If the polypeptide is not secreted, it can be recovered from cell lysates.

The medium used to culture the cells may be any conventional medium suitable for growing the host cells, such as minimal or complex media containing appropriate supplements. Suitable
10 able media are available from commercial suppliers or may be prepared according to published recipes (e.g. in catalogues of the American Type Culture Collection). The media are prepared using procedures known in the art (see, e.g., references for bacteria and yeast; Bennett, J.W. and LaSure, L., editors, *More Gene Manipulations in Fungi*, Academic Press, CA, 1991).

15 The polypeptides may be detected using methods known in the art that are specific for the polypeptides. These detection methods may include use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, an enzyme assay may be used to determine the activity of the polypeptide as described herein.

20 The resulting polypeptide may be recovered by methods known in the art. For example, the polypeptide may be recovered from the nutrient medium by conventional procedures including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation.

25 The polypeptides of the present invention may be purified by a variety of procedures known in the art including, but not limited to, chromatography (e.g., ion exchange, affinity, hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures (e.g., preparative isoelectric focusing), differential solubility (e.g., ammonium sulfate precipitation),
30 SDS-PAGE, or extraction (see, e.g., *Protein Purification*, J.-C. Janson and Lars Ryden, editors, VCH Publishers, New York, 1989).

A third aspect of the present invention relates to the use of a *Bacillus licheniformis* mutant host cell as defined in the first aspect for producing at least one product of interest
35 comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced, and optionally isolating or purifying the produced product.

The present invention is further illustrated by the following examples, which, however, are not to be construed as limiting the scope of protection. The features disclosed in the foregoing description and in the following examples may, both separately and in any combination thereof, be material for realising the invention in diverse forms thereof.

5

EXAMPLES

Example 1

10 The gene encoding a small extracellular protein from *B. licheniformis* is included in the sequence shown in SEQ ID NO: 133, where the start codon of the protein encoding sequence is the ATG in position 601, and the stopcodon is the TAA in position 979.

A vector designed to allow deletion of the entire open reading frame is constructed as follows:

15

1) An upstream DNA fragment is prepared by PCR amplification using chromosomal *B. licheniformis* DNA as template and the following primers:

EcoRI <L12 574-594> (SEQ ID NO: 201)

20 5'-gactgaattcgtgcgagttcctccacattcg-3'

HindIII BglII<L12 1074-1052> (SEQ ID NO: 202)

5'-gactaagcttagatctactctataagtttagtttgcacc-3'

25 The amplified fragment is digested with EcoRI og HindIII, inserted between the EcoRI and HindIII sites in pUC19, and the ligation mixture transformed into *E. coli* selecting ampicillin resistance (200 microg/ml).

30 2) The cloned DNA fragment is excised as an EcoRI-BglII fragment, and ligated to the 5.1 kb EcoRI-BglII fragment of pSJ2739 (Described in U.S. Patent 6,100,063, Fig. 10). The ligation mixture is transformed into *B. subtilis* DN1885 (Diderichsen et al., 1990 (Diderichsen, B., Wedsted, U., Hedegaard, L., Jensen, B. R., Sjøholm, C. (1990). Cloning of aldB, which encodes α -acetolactate decarboxylase, an exoenzyme from *Bacillus brevis*. J. Bacteriol. 172, 4315-4321)), selecting erythromycin resistance (5 microg/ml) at 30 °C.

35

3) A downstream DNA fragment is prepared by PCR amplification using chromosomal *B. licheniformis* DNA as template and the following primers:

KpnI BglII BamHI<L12 1500-1520> (SEQ ID NO: 203)
5'-gactggtaccagatctggatccgaaaacggttgctgtcaacgg-3'

5 HindIII<L12 2007-1986> (SEQ ID NO: 204)
5'-gactaagcttatcttttgtggagatgcttttg-3'

The amplified fragment is digested with KpnI and HindIII, and inserted into KpnI + HindIII digested pUC19. Transformation is into *E. coli*.

10

4) A DNA fragment containing a spectinomycin resistance gene (*spc*) flanked by resolvase sites (*res*) originating from plasmid pAMβ1 is excised as a 1.5 kb BclI-BamHI fragment from plasmid pSJ3358 (described in U.S. Patent 5,882,888), and inserted into the BamHI site of the plasmid constructed above, under 3). Transformation is into *E. coli*.

15

5) The entire "*res-spc-res*-downstream DNA fragment" segment is excised from the plasmid prepared under 4), above, using enzymes BglII and HindIII, and is inserted in the plasmid prepared under 2), above, which has been digested with BglII and HindIII. Transformation is into *B. subtilis* DN1885, selecting spectinomycin resistance (120 µg/ml) and erythromycin resistance (5 µg/ml) at 30 °C.

20

6) The plasmid constructed under 5), above, is transformed into donor strain PP289-5 (described in US 5,882,888) for easy transfer into *B. licheniformis* by conjugation.

25

B. licheniformis strains, which do not produce the small extracellular protein, are constructed by the following procedure:

30 The plasmid constructed under 5), above, is transferred into the *B. licheniformis* strain by conjugation from the *B. subtilis* donor strain constructed under 6), above, as described in US 5,882,888. Strains, in which the plasmid has integrated into the chromosome, are selected by isolation of colonies able to grow at 50 °C on plates containing erythromycin. Such colonies are then inoculated into liquid medium without antibiotics, and propagated overnight at 30 °C. These cultures are used to inoculate further liquid cultures, without antibiotics, again propagated overnight at 30 °C. If needed, this is repeated one or more

35

times. Aliquots from each overnight culture are spread on plates with spectinomycin (120 $\mu\text{g/ml}$) and incubated overnight at 30 °C, then replica plated onto plates with erythromycin (5 $\mu\text{g/ml}$). Colonies able to grow on spectinomycin, but sensitive to erythromycin, are picked and further investigated, e.g. by southern analysis and growth experiments. Such colonies
5 will have the chromosomal gene encoding the small extracellular protein replaced by the *res-spc-res* cassette.

The spectinomycin resistance gene may subsequently be deleted from the strain by introduction of a plasmid expressing the pAM β 1 resolvase gene, as described in US
10 5,882,888.

Alternatively, the *res-spc-res* cassette may be deleted in its entirety using a plasmid containing just the joined upstream and downstream regions flanking the gene for the extracellular protein, or such a plasmid may be used directly in the first step to delete the
15 gene for the extracellular protein in the *B. licheniformis* strain.

CLAIMS

1. A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more secreted polypeptide(s) which is at least 80% identical to one or more of the polypeptides shown in
5 SEQ ID NO's: 2 to 200, wherein the mutant host cell secretes at least 5% less of the one or more secreted polypeptide(s) than the parent host cell, when they are cultivated under comparable conditions.
2. The host cell according to claim 1, which is mutated by a partial or complete deletion of
10 the one or more gene(s) encoding the one or more secreted polypeptide(s).
3. The host cell according to claim 1 or 2, which is mutated by a partial or complete deletion of a gene encoding a secreted polypeptide which is at least 80% identical to the polypeptide shown in SEQ ID NO: 134.
15
4. The host cell according to any of claims 1 – 3, which is mutated in two or more genes encoding two or more secreted polypeptides.
5. The host cell according to any of claims 1 – 4, which comprises one or more heterologous
20 gene(s) encoding one or more heterologous polypeptide(s).
6. The host cell according to claim 5, wherein the heterologous gene(s) is present in at least two copies.
7. The host cell according to claim 5 or 6, wherein the heterologous gene(s) are stably
25 integrated into the genome of the cell.
8. The host cell according to any of claims 5 - 7, wherein the heterologous gene(s) is integrated into the genome of the cell without leaving any antibiotic resistance marker genes
30 at the site of integration.
9. The host cell according to any of claims 5 - 8, wherein the heterologous gene(s) are transcribed from a heterologous promoter or from an artificial promoter.
10. The host cell according to any of claim 5 – 9, wherein the heterologous gene(s) are
35 comprised in an operon, preferably a polycistronic operon.

11. The host cell according to any of claims 5 – 10, wherein the heterologous polypeptide(s) is an antimicrobial peptide, or a fusion peptide comprising a peptide part which in its native form has antimicrobial activity.

5 12. The host cell according to any of claims 5 – 10, wherein the heterologous polypeptide(s) has biosynthetic activity and produces a compound or an intermediate of interest.

13. The host cell according to claim 12, wherein the compound or intermediate of interest comprises vitamins, amino acids, antibiotics, carbohydrates, or surfactants.

10

14. The host cell according to claim 13, wherein the carbohydrates comprise hyaluronic acid.

15. The host cell according to any of claims 5 – 10, wherein the heterologous polypeptide(s) is an enzyme, preferably a secreted enzyme.

15

16. The host cell according to claim 15, wherein the enzyme is an enzyme of a class selected from the group of enzyme classes consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6).

20

17. The host cell according to claim 16, wherein the enzyme is an enzyme with an activity selected from the group of enzyme activities consisting of aminopeptidase, amylase, amyloglucosidase, mannanase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase, isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, and xylanase.

25

30 18. The host cell according to claim 17, wherein the enzyme is an amylase or a mannanase.

19. A process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in any of the claims 1 - 18 in a suitable medium, whereby the said product is produced.

35

20. The process according to claim 19, further comprising isolating or purifying the product of interest.

21. A use of a *Bacillus licheniformis* mutant host cell as defined in any of the claims 1 - 18 for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced.

5

22. The use according to claim 21 further comprising isolating or purifying the product of interest.

ABSTRACT

TITLE: Improved Bacillus Host Cell.

5 A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more secreted polypeptide(s) which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 200, wherein the mutant host cell secretes at least 5% less of the one or more secreted polypeptide(s) than the parent host cell, when they are cultivated under comparable conditions.

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Patent- og
Varemærkestyrelsen

10 APR. 2002

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Clausen, Ib Groth
Jørgensen, Steen Troels
Olsen, Peter Bjarke
Rasmussen, Michael Dølberg

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Ser Ala Lys Gly Lys Ser Ser Tyr Val Leu Thr Glu Asp Pro Phe Ile
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Val Glu

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<220>

<221> CDS

<222> (501)..(2573)

<223>

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gattttctc ggcttggcgg gagtgctgat cgcaaagaaa gagcagcttg ctctatggct	180
gccgcttgcg tggtcctcgg gtttaatgct ctttttcaaa ttcaatatat cctttaaagg	240
gctgctcccg ggggaaggca tgctgttgct catccatgca gcaggagctt ccccgattct	300
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ttg ctg cgt ttg acg ccg gag caa gcg gaa aca ggc ggc tac aac gta Leu Leu Arg Leu Thr Pro Glu Gln Ala Glu Thr Gly Gly Tyr Asn Val 285 290 295	1397
ttc acc acg ctc aac ccg cgt ctc caa aaa att gcc gag gat acg atc Phe Thr Thr Leu Asn Pro Arg Leu Gln Lys Ile Ala Glu Asp Thr Ile 300 305 310 315	1445
gaa cac acg ata gat tcg tca tcc gac att cag gcg gga ttt gca gcg Glu His Thr Ile Asp Ser Ser Ser Asp Gln Ala Gly Phe Ala Ala 320 325 330	1493
atc aac ccg tcc gac ggc agc gtt ctc gcg ctt gtc gga gga cgc gac Ile Asn Pro Ser Asp Gly Ser Val Leu Ala Leu Val Gly Gly Arg Asp 335 340 345	1541
tac gaa aaa agc cct ttt aac cgc gta acg cag gct atg cgg cag ccc Tyr Glu Lys Ser Pro Phe Asn Arg Val Thr Gln Ala Met Arg Gln Pro 350 355 360	1589
ggc tcc acc atg aag cct ttc ctt tat tat tcg gcg gtt caa aac ggc Gly Ser Thr Met Lys Pro Phe Leu Tyr Tyr Ser Ala Val Gln Asn Gly 365 370 375	1637
ttt aca ccg gcc acc cga atg agg agc gcg gaa acg aca ttt gag ctc Phe Thr Pro Ala Thr Arg Met Arg Ser Ala Glu Thr Thr Phe Glu Leu 380 385 390 395	1685
ggg caa ggc agc gct tat tcc ccg agc aac tat cac ggc tat tat gca Gly Gln Gly Ser Ala Tyr Ser Pro Ser Asn Tyr His Gly Tyr Tyr Ala 400 405 410	1733
gac ggt ccg atc acg ctt ctg cag gca ctg gct ttg tcc gat aac att Asp Gly Pro Ile Thr Leu Leu Gln Ala Leu Ala Leu Ser Asp Asn Ile 415 420 425	1781
tac gcc gtg aaa acc cac ctt ttc ctc ggc atg gac aaa ctg att gat Tyr Ala Val Lys Thr His Leu Phe Leu Gly Met Asp Lys Leu Ile Asp 430 435 440	1829
gcc gca aag caa ttc ggc atc aac agc ccg ctg caa aaa gtg ccg tcg Ala Ala Lys Gln Phe Gly Ile Asn Ser Pro Leu Gln Lys Val Pro Ser 445 450 455	1877
ctt gcg ctc gga aca tcc cct gtg aag ccg att gaa atg gtg aac gga Leu Ala Leu Gly Thr Ser Pro Val Lys Pro Ile Glu Met Val Asn Gly 460 465 470 475	1925
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acg aaa att acc gat ccg aac ggc aag gtt ctt tat gaa aaa ccg aag Thr Lys Ile Thr Asp Pro Asn Gly Lys Val Leu Tyr Glu Lys Pro Lys 495 500 505	2021
cgg agc aaa caa atc ctt gac cca aaa gcg gct ttt atc acg gcg aac Arg Ser Lys Gln Ile Leu Asp Pro Lys Ala Ala Phe Ile Thr Ala Asn 510 515 520	2069
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ctt gct tca ggc gtg tgg acg gga tat gac aaa gag cgg aca atc gat Leu Ala Ser Gly Val Trp Thr Gly Tyr Asp Lys Glu Arg Thr Ile Asp 575 580 585	2261
gcc gtc gca gag aaa aac tat gcc aaa caa att tgg gct gag ttt atg Ala Val Ala Glu Lys Asn Tyr Ala Lys Gln Ile Trp Ala Glu Phe Met 590 595 600	2309
gaa aaa gcg ctt gaa gac gcg ccc gcc gca gct tta atg ccg cct gaa Glu Lys Ala Leu Glu Asp Ala Pro Ala Ala Ala Leu Met Pro Pro Glu 605 610 615	2357
ggc gtg aaa ggg atg tac atc gac ccg gct aca ggt tat gcg gcg gcg Gly Val Lys Gly Met Tyr Ile Asp Pro Ala Thr Gly Tyr Ala Ala Ala 620 625 630 635	2405
ccc agc tgc ccg tcc aaa tat ttc gct tat ttt atc aaa ggt act gaa Pro Ser Cys Pro Ser Lys Tyr Phe Ala Tyr Phe Ile Lys Gly Thr Glu 640 645 650	2453
ccc gag cag gtt tgc tat gga aag gaa atc tat aag gag caa aac gcc Pro Glu Gln Val Cys Tyr Gly Lys Glu Ile Tyr Lys Glu Gln Asn Ala 655 660 665	2501
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<212> PRT

<213> Bacillus licheniformis

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 Val Val Met Thr Val Val Leu Ala Ala Lys Trp Gln Gly Ala Pro Ser
 35 40 45
 Ile Gln Val Pro Arg Ser Thr Val Leu Tyr Asp Gly Ser Gly Lys Gln
 50 55 60
 Met Gly Glu Thr His Tyr Gly Gln Lys Arg Tyr Trp Val Ser Leu Lys
 65 70 75 80
 Asn Ile Asn Pro Ala Val Ile Asp Ala Thr Leu Ala Val Glu Asp Arg
 85 90 95
 Asn Phe Phe Arg His His Gly Phe Asp Tyr Met Arg Met Gly Gly Ala
 100 105 110
 Leu Ile Ala Asp Leu Lys Ala Met Ser Lys Val Gln Gly Ala Ser Thr
 115 120 125
 Ile Thr Gln Gln Tyr Ala Arg Asn Leu Tyr Leu Gly His Asp Lys Thr
 130 135 140
 Trp Lys Arg Lys Trp Asn Glu Ala Phe Tyr Thr Ile Arg Leu Glu Gln
 145 150 155 160
 Asn Tyr Thr Lys Lys Asp Ile Leu Glu Gly Tyr Leu Asn Thr Ile Tyr
 165 170 175
 Tyr Gly His Gly Ala Tyr Gly Ile Glu Ala Ala Ser Arg Leu Tyr Phe
 180 185 190
 Gly Lys Arg Ala Lys Asp Ile Asn Thr Ala Glu Ala Ala Met Leu Ala
 195 200 205
 Gly Ile Pro Lys Gly Pro Ser Val Tyr Ser Pro Phe Val Asn Glu Lys
 210 215 220
 Lys Ala Lys Glu Arg Gln Glu Met Ile Leu Thr Met Met Glu Lys Gln
 225 230 235 240
 Asn Lys Leu Thr Glu Met Gln Ala Ala Ala Leu Lys Lys Met Pro Leu
 245 250 255
 Arg Phe Glu Lys Gln Asp Lys Gln Thr Thr Glu Lys Thr Ala Pro Tyr
 260 265 270
 Phe Tyr Asp Glu Ala Val Lys Glu Ile Ser Arg Leu Leu Arg Leu Thr
 275 280 285

Pro Glu Gln Ala Glu Thr Gly Gly Tyr Asn Val Phe Thr Thr Leu Asn
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 Pro Arg Leu Gln Lys Ile Ala Glu Asp Thr Ile Glu His Thr Ile Asp
 305 310 315 320
 Ser Ser Ser Asp Ile Gln Ala Gly Phe Ala Ala Ile Asn Pro Ser Asp
 325 330 335
 Gly Ser Val Leu Ala Leu Val Gly Gly Arg Asp Tyr Glu Lys Ser Pro
 340 345 350
 Phe Asn Arg Val Thr Gln Ala Met Arg Gln Pro Gly Ser Thr Met Lys
 355 360 365
 Pro Phe Leu Tyr Tyr Ser Ala Val Gln Asn Gly Phe Thr Pro Ala Thr
 370 375 380
 Arg Met Arg Ser Ala Glu Thr Thr Phe Glu Leu Gly Gln Gly Ser Ala
 385 390 395 400
 Tyr Ser Pro Ser Asn Tyr His Gly Tyr Tyr Ala Asp Gly Pro Ile Thr
 405 410 415
 Leu Leu Gln Ala Leu Ala Leu Ser Asp Asn Ile Tyr Ala Val Lys Thr
 420 425 430
 His Leu Phe Leu Gly Met Asp Lys Leu Ile Asp Ala Ala Lys Gln Phe
 435 440 445
 Gly Ile Asn Ser Pro Leu Gln Lys Val Pro Ser Leu Ala Leu Gly Thr
 450 455 460
 Ser Pro Val Lys Pro Ile Glu Met Val Asn Gly Tyr Ala Met Phe Ala
 465 470 475 480
 Asn Gly Gly Lys Lys Ile Glu Pro Ser Phe Ile Thr Lys Ile Thr Asp
 485 490 495
 Pro Asn Gly Lys Val Leu Tyr Glu Lys Pro Lys Arg Ser Lys Gln Ile
 500 505 510
 Leu Asp Pro Lys Ala Ala Phe Ile Thr Ala Asn Met Met Ser Gly Met
 515 520 525
 Phe Asp Lys Ser Leu Asn Gly Tyr Thr Ser Val Thr Gly Arg Thr Ile
 530 535 540
 Ala Asp Gln Leu Thr Arg Arg Tyr Ala Gly Lys Ser Gly Thr Thr Ser
 545 550 555 560

Thr Asp Ser Trp Met Ile Gly Phe Tyr Pro Gly Leu Ala Ser Gly Val
565 570 575

Trp Thr Gly Tyr Asp Lys Glu Arg Thr Ile Asp Ala Val Ala Glu Lys
580 585 590

Asn Tyr Ala Lys Gln Ile Trp Ala Glu Phe Met Glu Lys Ala Leu Glu
595 600 605

Asp Ala Pro Ala Ala Ala Leu Met Pro Pro Glu Gly Val Lys Gly Met
610 615 620

Tyr Ile Asp Pro Ala Thr Gly Tyr Ala Ala Ala Pro Ser Cys Pro Ser
625 630 635 640

Lys Tyr Phe Ala Tyr Phe Ile Lys Gly Thr Glu Pro Glu Gln Val Cys
645 650 655

Tyr Gly Lys Glu Ile Tyr Lys Glu Gln Asn Ala Gly His Glu Lys Pro
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Lys Gly Glu
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<220>

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gtcatcggcc cggtgctcgg cggcatcctt tccagctttt tcggtatttc ttccgccttt 180
tacgcaactg cagtcctctt ttctggcgga gcatgccttc tgatgttcca aagggtcccag 240
caaaaaaat cagaggcgaa agcaagctga aatcggataa aaaaactgcc aatctatcaa 300

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a gtg aca aag ttg cgt tca ttt ttt gga tgg att ttt ctg ttg atg tta 409
Val Thr Lys Leu Arg Ser Phe Phe Gly Trp Ile Phe Leu Leu Met Leu
1 5 10 15

ata cct ata ttt gtc ttt acc tta atg gcc tcc ggc cgg gaa gct cag 457
Ile Pro Ile Phe Val Phe Thr Leu Met Ala Ser Gly Arg Glu Ala Gln
20 25 30

aat atg aag cct ctc gat cag gtg ctc gat gag aag atc aat ata aag 505
Asn Met Lys Pro Leu Asp Gln Val Leu Asp Glu Lys Ile Asn Ile Lys
35 40 45

gat atc ggc ctt gta caa aac agc tac atg tat gac agg gac ggc gct 553
Asp Ile Gly Leu Val Gln Asn Ser Tyr Met Tyr Asp Arg Asp Gly Ala
50 55 60

ctg att tcc gaa atc gtt tca gat cac caa aac cgg gta ttc gtc ccc 601
Leu Ile Ser Glu Ile Val Ser Asp His Gln Asn Arg Val Phe Val Pro
65 70 75 80

tat aaa gat atc cct gaa cat gtg aag cag ctg ttt ctg act tcg gag 649
Tyr Lys Asp Ile Pro Glu His Val Lys Gln Leu Phe Leu Thr Ser Glu
85 90 95

gac cgt cat ttc ttt cag cat aaa ggc ttt gat ttt atc ggg atg gcc 697
Asp Arg His Phe Phe Gln His Lys Gly Phe Asp Phe Ile Gly Met Ala
100 105 110

cgg gcc gcc gca gcc aat gtc aaa aaa ggc ggc att gat cag ggg gcc 745
Arg Ala Ala Ala Asn Val Lys Lys Gly Gly Ile Asp Gln Gly Ala
115 120 125

agc acg att aca cag cag ctt tcg aga aac ttg tat ttg aac cat gaa 793
Ser Thr Ile Thr Gln Gln Leu Ser Arg Asn Leu Tyr Leu Asn His Glu
130 135 140

cga acc ttc gac cgc aag ttc act gag ctc ctg tat tcc tac cag ctg 841
Arg Thr Phe Asp Arg Lys Phe Thr Glu Leu Leu Tyr Ser Tyr Gln Leu
145 150 155 160

gaa aaa aag ctt tca aaa gaa gaa att ttt gag aaa tac tta aac acc 889
Glu Lys Lys Leu Ser Lys Glu Glu Ile Phe Glu Lys Tyr Leu Asn Thr
165 170 175

atc tat ttt aat cac ggg gtc tac gga att gga tcc gcg tct tct ttc 937
Ile Tyr Phe Asn His Gly Val Tyr Gly Ile Gly Ser Ala Ser Ser Phe
180 185 190

tat ttc agc aag cct ttg aaa tct ctc agc ctt gcc gaa acg gcg ttt 985
Tyr Phe Ser Lys Pro Leu Lys Ser Leu Ser Leu Ala Glu Thr Ala Phe
195 200 205

att tgc gcg atc cct aat aac cct aca tta tat gat cct ttg aaa cat 1033
Ile Cys Ala Ile Pro Asn Asn Pro Thr Leu Tyr Asp Pro Leu Lys His
210 215 220

ttt gac tac aca aaa acc cgc caa aag cgg ctg ctt gaa ggg ctg aaa 1081
Phe Asp Tyr Thr Lys Thr Arg Gln Lys Arg Leu Leu Glu Gly Leu Lys
225 230 235 240

aaa gcg ggc gtg atc acc gaa aaa gaa tac agc aaa gcc gtt aag caa 1129
Lys Ala Gly Val Ile Thr Glu Lys Glu Tyr Ser Lys Ala Val Lys Gln
245 250 255

aaa att acg ctt aac gtg aaa gaa aag aaa gac gac tat ccc gac tat 1177

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Thr	Thr	Tyr	Val	Asn	Glu	Glu	Phe	Thr	Lys	Leu	Val	Ser	Ala	Thr	Glu	
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Gly	Phe	Asp	Glu	Arg	Leu	Lys	Lys	Ala	Lys	Thr	Lys	Glu	Glu	Lys	Lys	
	290					295					300					
aaa	atc	gaa	aaa	gag	ctg	tca	aac	cga	atc	agc	tcc	ctc	acg	aca	agc	1321
Lys	Ile	Glu	Lys	Glu	Leu	Ser	Asn	Arg	Ile	Ser	Ser	Leu	Thr	Thr	Ser	
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Gly	Ile	Lys	Ile	Tyr	Thr	Ala	Leu	Asp	Thr	Ser	Met	Gln	Asn	Arg	Val	
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gtc	cag	caa	gtg	aag	aac	cgc	ctc	cct	tat	gaa	ggc	gta	caa	ggc	gga	1417
Val	Gln	Gln	Val	Lys	Asn	Arg	Leu	Pro	Tyr	Glu	Gly	Val	Gln	Gly	Gly	
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gca	gtg	gtg	atc	aac	cac	caa	acc	cat	caa	atc	gtc	gcc	atg	tcc	ggc	1465
Ala	Val	Val	Ile	Asn	His	Gln	Thr	His	Gln	Ile	Val	Ala	Met	Ser	Gly	
		355					360					365				
ggg	aaa	aac	tat	aaa	aag	tac	gat	tat	aac	ctg	gca	ttc	caa	gca	tac	1513
Gly	Lys	Asn	Tyr	Lys	Lys	Tyr	Asp	Tyr	Asn	Leu	Ala	Phe	Gln	Ala	Tyr	
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agg	cag	ccg	ggg	tca	tca	att	aag	ccg	ctc	ctt	gac	tac	ggg	ccg	tac	1561
Arg	Gln	Pro	Gly	Ser	Ser	Ile	Lys	Pro	Leu	Leu	Asp	Tyr	Gly	Pro	Tyr	
385					390					395					400	
att	gaa	gaa	acg	ggt	gcg	acg	gca	ggc	agc	atg	att	gac	gca	agc	aaa	1609
Ile	Glu	Glu	Thr	Gly	Ala	Thr	Ala	Gly	Ser	Met	Ile	Asp	Ala	Ser	Lys	
				405					410					415		
ttt	tgc	agc	aag	gaa	tac	tgt	ccg	aac	aac	ttc	aac	gaa	aga	aca	tac	1657
Phe	Cys	Ser	Lys	Glu	Tyr	Cys	Pro	Asn	Asn	Phe	Asn	Glu	Arg	Thr	Tyr	
			420					425					430			
gga	acc	gtg	tcg	atc	aag	aca	gcc	ttt	aaa	tat	tcg	tat	aat	aca	cca	1705
Gly	Thr	Val	Ser	Ile	Lys	Thr	Ala	Phe	Lys	Tyr	Ser	Tyr	Asn	Thr	Pro	
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Ala	Val	Arg	Met	Leu	Asn	Arg	Val	Gly	Val	Gln	Lys	Gly	Phe	Ser	Tyr	
	450					455					460					
tta	aaa	ccg	ttc	gga	ttc	gat	aaa	atc	gtt	caa	aac	gac	tac	cgt	ctt	1801
Leu	Lys	Pro	Phe	Gly	Phe	Asp	Lys	Ile	Val	Gln	Asn	Asp	Tyr	Arg	Leu	
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cct	gct	gcg	ctg	ggc	gga	ttt	aca	tgg	ggc	ttc	tca	ccg	ctg	gag	atg	1849
Pro	Ala	Ala	Leu	Gly	Gly	Phe	Thr	Trp	Gly	Phe	Ser	Pro	Leu	Glu	Met	
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gct	gat	gcc	tat	acg	acc	ttc	ggc	aat	aac	gga	agc	tac	aca	tcc	agc	1897
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His	Ala	Ile	Thr	Lys	Val	Thr	Asp	Leu	Lys	Gly	Lys	Thr	Leu	Tyr	Lys	
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atg cgc gaa ctc tta gca gcg gtt gtt aaa gaa gga acc gga aaa aaa 2041
 Met Arg Glu Leu Leu Ala Ala Val Val Lys Glu Gly Thr Gly Lys Lys
 545 550 555 560

gcg aat ttc agc ggc gga tat gta gga gga aaa acc gga aca tcc aac 2089
 Ala Asn Phe Ser Gly Gly Tyr Val Gly Gly Lys Thr Gly Thr Ser Asn
 565 570 575

ggg tac aga gac ctt tgg ttt gtc gga ttg acg gat aca tac aca atg 2137
 Gly Tyr Arg Asp Leu Trp Phe Val Gly Leu Thr Asp Thr Tyr Thr Met
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agt gta tgg gtc gga aaa gag gca aaa ggc act gtc gag tac ctg cat 2185
 Ser Val Trp Val Gly Lys Glu Ala Lys Gly Thr Val Glu Tyr Leu His
 595 600 605

cac gcg gga cct caa ctt tta atc tgg aga gga acg ctg caa tac gca 2233
 His Ala Gly Pro Gln Leu Leu Ile Trp Arg Gly Thr Leu Gln Tyr Ala
 610 615 620

tct taaattaaaa aaaggggtgg atgaaagtgg cggatatgcc cgatcgaatc 2286
 Ser
 625

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aagcaatatc acctcccttc cgatcatttt aacagcttta ttttgatcga aaacggcccg 2466

gtatatcaaa agtcaacggc cgccttgcac gtgggtgaaaa gcctcccggg cttttggcgg 2526

gccgcttccg ccctcttgat cattccccgg ccgcttcggg acgccgtcta cagtgtcatt 2586

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<213> Bacillus licheniformis

<400> 6

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Asn Met Lys Pro Leu Asp Gln Val Leu Asp Glu Lys Ile Asn Ile Lys
 35 40 45

Asp Ile Gly Leu Val Gln Asn Ser Tyr Met Tyr Asp Arg Asp Gly Ala
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 Leu Ile Ser Glu Ile Val Ser Asp His Gln Asn Arg Val Phe Val Pro
 65 70 75 80
 Tyr Lys Asp Ile Pro Glu His Val Lys Gln Leu Phe Leu Thr Ser Glu
 85 90 95
 Asp Arg His Phe Phe Gln His Lys Gly Phe Asp Phe Ile Gly Met Ala
 100 105 110
 Arg Ala Ala Ala Ala Asn Val Lys Lys Gly Gly Ile Asp Gln Gly Ala
 115 120 125
 Ser Thr Ile Thr Gln Gln Leu Ser Arg Asn Leu Tyr Leu Asn His Glu
 130 135 140
 Arg Thr Phe Asp Arg Lys Phe Thr Glu Leu Leu Tyr Ser Tyr Gln Leu
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 Glu Lys Lys Leu Ser Lys Glu Glu Ile Phe Glu Lys Tyr Leu Asn Thr
 165 170 175
 Ile Tyr Phe Asn His Gly Val Tyr Gly Ile Gly Ser Ala Ser Ser Phe
 180 185 190
 Tyr Phe Ser Lys Pro Leu Lys Ser Leu Ser Leu Ala Glu Thr Ala Phe
 195 200 205
 Ile Cys Ala Ile Pro Asn Asn Pro Thr Leu Tyr Asp Pro Leu Lys His
 210 215 220
 Phe Asp Tyr Thr Lys Thr Arg Gln Lys Arg Leu Leu Glu Gly Leu Lys
 225 230 235 240
 Lys Ala Gly Val Ile Thr Glu Lys Glu Tyr Ser Lys Ala Val Lys Gln
 245 250 255
 Lys Ile Thr Leu Asn Val Lys Glu Lys Lys Asp Asp Tyr Pro Asp Tyr
 260 265 270
 Thr Thr Tyr Val Asn Glu Glu Phe Thr Lys Leu Val Ser Ala Thr Glu
 275 280 285
 Gly Phe Asp Glu Arg Leu Lys Lys Ala Lys Thr Lys Glu Glu Lys Lys
 290 295 300
 Lys Ile Glu Lys Glu Leu Ser Asn Arg Ile Ser Ser Leu Thr Thr Ser
 305 310 315 320

Gly Ile Lys Ile Tyr Thr Ala Leu Asp Thr Ser Met Gln Asn Arg Val
 325 330 335

Val Gln Gln Val Lys Asn Arg Leu Pro Tyr Glu Gly Val Gln Gly Gly
 340 345 350

Ala Val Val Ile Asn His Gln Thr His Gln Ile Val Ala Met Ser Gly
 355 360 365

Gly Lys Asn Tyr Lys Lys Tyr Asp Tyr Asn Leu Ala Phe Gln Ala Tyr
 370 375 380

Arg Gln Pro Gly Ser Ser Ile Lys Pro Leu Leu Asp Tyr Gly Pro Tyr
 385 390 395 400

Ile Glu Glu Thr Gly Ala Thr Ala Gly Ser Met Ile Asp Ala Ser Lys
 405 410 415

Phe Cys Ser Lys Glu Tyr Cys Pro Asn Asn Phe Asn Glu Arg Thr Tyr
 420 425 430

Gly Thr Val Ser Ile Lys Thr Ala Phe Lys Tyr Ser Tyr Asn Thr Pro
 435 440 445

Ala Val Arg Met Leu Asn Arg Val Gly Val Gln Lys Gly Phe Ser Tyr
 450 455 460

Leu Lys Pro Phe Gly Phe Asp Lys Ile Val Gln Asn Asp Tyr Arg Leu
 465 470 475 480

Pro Ala Ala Leu Gly Gly Phe Thr Trp Gly Phe Ser Pro Leu Glu Met
 485 490 495

Ala Asp Ala Tyr Thr Thr Phe Gly Asn Asn Gly Ser Tyr Thr Ser Ser
 500 505 510

His Ala Ile Thr Lys Val Thr Asp Leu Lys Gly Lys Thr Leu Tyr Lys
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Met Lys Arg Phe Leu Gln Cys Ala Leu Ile Ala
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 Val Pro His Asn Glu Lys Arg Leu Arg Ser Val Glu Leu Ala Pro Phe
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Asp	Ser	Asn	Tyr	Ser	Met	Ala	Val	Phe	Ala	Pro	Phe	Lys	Gly	Gln	Gly	
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atc ata gcg gca gcg gtt att ttg atc ttg aca acg gca agg cgc aga 2597
 ile ile Ala Ala Ala Val Ile Leu Ile Leu Thr Thr Ala Arg Arg Arg
 685 690 695

aaa aga aag gcc aat gcc ggc gga ggg att gac gaa taaaacaggg 2643
 Lys Arg Lys Ala Asn Ala Gly Gly Gly Ile Asp Glu
 700 705 710

gcttgctttt agcccctgtt tttttataag tattcaacct gtttctcata tacacccttc 2703
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 35 40 45

Leu Thr Asn Asp Leu Leu Thr Leu Tyr Gly Ala Lys Asp Ser Ala Glu
 50 55 60

Leu Thr Tyr Gln Ile Pro Ala Gly Ala Ser Ser Thr His Gln Gln Leu
 65 70 75 80

Thr Leu Lys Tyr Glu Ala Ser Asp Leu Leu Ile Ser Pro Ser Ser Leu
 85 90 95

Thr Ala Glu Ile Asp Gly Glu Pro Val Lys Thr Val Lys Leu Glu Gly
 100 105 110

Asn Asn Gly Lys Lys Thr Leu Lys Leu Ser Leu Asn Lys Ser Gln Ser
 115 120 125

Ser Pro Gly Phe His Ser Leu Ser Leu Lys Phe Tyr Gly Val Val His
 130 135 140

Glu Gly Val Cys Val Arg Gln Asp Ser Ser Gly Asn Trp Ile Lys Ile
 145 150 155 160

Tyr Pro Asp Ser Arg₁₆₅ Leu Asn Ile Gly₁₇₀ Glu Lys Asn Glu Ser₁₇₅ Lys Gly
 Ala Ala Leu Glu₁₈₀ His Tyr Pro Tyr₁₈₅ Phe Ala Gln Ser₁₉₀ Gly Ser Ser
 Val Glu Lys₁₉₅ Thr Ala Ile Val₂₀₀ Ile Pro Asp His Pro₂₀₅ Ser Ser Ala Glu
 Ile Glu₂₁₀ Ala Ala Val Lys₂₁₅ Thr Glu Ala Tyr Leu Lys₂₂₀ Thr Val Asp Asn
 Ser₂₂₅ Ile Ser Thr Lys₂₃₀ Ile Leu Gly Glu Ser₂₃₅ Asp Leu Ala Lys Ile Asp₂₄₀
 Arg Pro Thr Ile Val₂₄₅ Ile Gly Val His₂₅₀ His Trp Ser Gly₂₅₅ Lys Val
 Lys Lys Leu₂₆₀ Lys Glu Ala Lys₂₆₅ Glu Ala Lys Glu Asp₂₇₀ Lys Leu
 Leu Leu Ala₂₇₅ Lys Arg Met Leu₂₈₀ Lys Ala Lys Asp Lys₂₈₅ Gln Gln Pro Val
 Leu Phe₂₉₀ Ala Ala Ala Ala Ser₂₉₅ Asp Asp Val Leu₃₀₀ Ser Glu Lys Ile Ser
 Val₃₀₅ Ile Thr Asp Lys₃₁₀ Thr Tyr Ala Ala Gln Leu₃₁₅ Ser Gly Asp Thr Leu₃₂₀
 Ala Ile Gly Lys₃₂₅ Leu Gln Gln His Ser₃₃₀ Lys Arg Gly Gly Ser₃₃₅ Lys Leu
 Thr Leu Glu Asp₃₄₀ Phe Gly Ala Gly₃₄₅ Asp Leu Thr Ile Gly Ser₃₅₀ Gly Gln
 Thr Ser Ser₃₅₅ Glu His Phe Tyr₃₆₀ Pro Ala Pro Ala Leu₃₆₅ Leu Asp Lys
 Asn Gln₃₇₀ Pro Ala Lys Leu Ser₃₇₅ Leu Ala Met Lys₃₈₀ Lys Ser Lys Thr Ile
 Gln Lys Gln Ala Gly₃₉₀ Gln Ser Asp Leu Ala₃₉₅ Glu Gln Ala Glu Leu₄₀₀
 Lys Val Met Ile Asn₄₀₅ Gly Gln Pro His Ser₄₁₀ Val Gly Leu Asp₄₁₅ Asp Ile
 Gly Lys Glu Asp₄₂₀ Lys Asn Gly Phe Tyr₄₂₅ His Val Ser Leu Lys₄₃₀ Val Asp

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Pro Lys Leu₄₃₅ Leu Gln Lys Ser Arg₄₄₀ Tyr Ile Asp Ile Gln₄₄₅ Phe Ala Ala
 Ser Gly₄₅₀ Leu Lys Glu Asn Asn₄₅₅ Pro Cys Tyr Ala Val₄₆₀ Asn Glu Asp Lys
 Trp₄₆₅ Ile Phe Ile Asp Lys₄₇₀ Gln Ser Ala Leu Ser₄₇₅ Tyr His Val Ser Asp₄₈₀
 Thr Ser Ala Ser Ala₄₈₅ Asp Phe Gln Ala Trp₄₉₀ Pro Leu Pro Tyr Ala₄₉₅ Gly
 Asp His Asn Asn₅₀₀ Lys Thr Leu Met Ile₅₀₅ Leu Pro Asp Asn Ala₅₁₀ Asp Gln
 Ser Lys Ile₅₁₅ Asp Glu Leu Ser Leu₅₂₀ Val Val Gly Ser Phe₅₂₅ Gly Ser Glu
 Ala Arg₅₃₀ Gln Ala Phe Thr Val₅₃₅ Lys Thr Ser Ser Glu₅₄₀ Val Lys Pro Asp
 Asp Val₅₄₅ Lys Gly Arg Asn₅₅₀ Val Ile Phe Ile Gly₅₅₅ Ser Val Asp Gln Phe₅₆₀
 Ser Leu Leu Lys Glu₅₆₅ Lys Thr Ala Glu Leu₅₇₀ Ala Val Pro Thr Ala₅₇₅ Lys
 Asn Gly Thr Phe₅₈₀ Asp Val Ser Ser Phe₅₈₅ Gln Met Leu Asn Glu₅₉₀ Thr Thr
 Lys Gln Val₅₉₅ Ala Phe Thr Gln Thr₆₀₀ Ser Leu Trp Asp Ser₆₀₅ Asn Tyr Ser
 Met Ala₆₁₀ Val Phe Ala Pro Phe₆₁₅ Lys Gly Gln Gly Thr₆₂₀ Ala Val Thr Lys
 Glu Met Ile Asn Phe Leu₆₃₀ Asn Ser Asn Asp Phe₆₃₅ Ala Ala Thr Val Val₆₄₀
 Asn Glu Thr Asp Ser₆₄₅ His Gln Leu Phe Thr₆₅₀ Asn His Gln Gln Leu Thr₆₅₅
 Ala Lys Ser Ala₆₆₀ Glu Thr Lys Thr Asp₆₆₅ Asp Lys Gln Glu Ser₆₇₀ Asn Gln
 Gln His Val₆₇₅ Leu Tyr Ile Ala Ile₆₈₀ Leu Ile Val Ile Ile₆₈₅ Ala Ala Ala
 Val Ile₆₉₀ Leu Ile Leu Thr Thr₆₉₅ Ala Arg Arg Arg Lys₇₀₀ Arg Lys Ala Asn

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<213> Bacillus licheniformis

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<222> (519)..(1958)
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atccatctat gtttgagcct gtgcacggct ctgctccgga catcatctga tagcgagtca 180
tcacgcgaaa aggaatcgcc aatccgatcg gccaaatttg gacggcaaaa atgatgctcg 240
atcatttcgg ggaagaagaa ctcggtgcaa gattgcttga cgtgattgaa gacgttctaa 300
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gcaacaaaac atagtgcagg cagaagagga ggtatagg atg aat cag aag att gtg 536
Met Asn Gln Lys Ile Val
1 5
tct gtg ctc atc att gcg ctc agc ctg tta tgc ggc ttg gta aca ggc 584
Ser Val Leu Ile Ile Ala Leu Ser Leu Leu Cys Gly Leu Val Thr Gly
10 15 20
gcc ggc ccg att ccg tta cat gat gtc gtt tca aaa gca tca gcg gct 632
Ala Gly Pro Ile Pro Leu His Asp Val Val Ser Lys Ala Ser Ala Ala
25 30 35
gaa gaa gct gca gcc aaa agc acc gct aga aac gaa ttg gag aaa att 680
Glu Glu Ala Ala Ala Lys Ser Thr Ala Arg Asn Glu Leu Glu Lys Ile
40 45 50
gag aaa gca tat gac ctg att tca aat gaa tat gtg gag cag gtc gac 728
Glu Lys Ala Tyr Asp Leu Ile Ser Asn Glu Tyr Val Glu Gln Val Asp
55 60 65 70
agg gaa aaa ctg ttg gaa gga gcc ata cag ggc atg ctt tca aca ttg 776
Arg Glu Lys Leu Leu Glu Gly Ala Ile Gln Gly Met Leu Ser Thr Leu
75 80 85
aat gac cca tac tcg gtc tat atg gat aaa cag acg gca aag cgg ttt 824

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Ser	Asp	Ser	Leu	Asp	Ser	Ser	Phe	Glu	Gly	Ile	Gly	Ala	Glu	Ile	Gly	
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Met	Glu	Asp	Arg	Lys	Ile	Ile	Ile	Val	Ser	Pro	Phe	Lys	Gln	Ser	Pro	
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Ala	Glu	Lys	Ala	Gly	Leu	Lys	Pro	Asn	Asp	Glu	Ile	Ile	Ser	Ile	Asp	
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ggc	gat	tcc	atg	agc	gga	atg	gat	ttg	aat	gac	gcc	gta	tta	aag	atc	1016
Gly	Asp	Ser	Met	Ser	Gly	Met	Asp	Leu	Asn	Asp	Ala	Val	Leu	Lys	Ile	
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Arg	Gly	Lys	Lys	Gly	Ser	Thr	Val	Thr	Leu	Lys	Val	His	Arg	Pro	Gly	
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Met	Lys	Asp	Gln	Leu	Thr	Phe	Thr	Ile	Lys	Arg	Asp	Glu	Ile	Pro	Leu	
		185					190					195				
gaa	acg	gtg	ttt	gct	tcc	ata	aag	aaa	gta	cag	gat	aaa	cct	gtc	ggc	1160
Glu	Thr	Val	Phe	Ala	Ser	Ile	Lys	Lys	Val	Gln	Asp	Lys	Pro	Val	Gly	
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tat	atc	gca	ata	tct	tcc	ttt	tcc	gaa	cat	acg	gca	aaa	gat	ttt	act	1208
Tyr	Ile	Ala	Ile	Ser	Ser	Phe	Ser	Glu	His	Thr	Ala	Lys	Asp	Phe	Thr	
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gct	gaa	ctg	aaa	aag	ctt	gag	aaa	aag	gga	ata	aaa	ggg	ctc	gtt	ttg	1256
Ala	Glu	Leu	Lys	Lys	Leu	Glu	Lys	Lys	Gly	Ile	Lys	Gly	Leu	Val	Leu	
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gat	gta	aga	gga	aat	ccg	ggc	ggg	tac	ttg	caa	agc	gtg	gaa	gac	att	1304
Asp	Val	Arg	Gly	Asn	Pro	Gly	Gly	Tyr	Leu	Gln	Ser	Val	Glu	Asp	Ile	
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tta	aaa	cat	ttt	gtg	aca	aaa	gat	cat	ccg	tat	ata	caa	atc	gcc	gaa	1352
Leu	Lys	His	Phe	Val	Thr	Lys	Asp	His	Pro	Tyr	Ile	Gln	Ile	Ala	Glu	
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cca	tac	cct	gtg	agc	gtg	atc	acg	gac	aag	ggc	agc	gct	tcg	gct	tcg	1448
Pro	Tyr	Pro	Val	Ser	Val	Ile	Thr	Asp	Lys	Gly	Ser	Ala	Ser	Ala	Ser	
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gaa	att	ctt	gca	ggc	gca	tta	aaa	gaa	gcc	gag	ggc	tac	gac	gtg	gtt	1496
Glu	Ile	Leu	Ala	Gly	Ala	Leu	Lys	Glu	Ala	Glu	Gly	Tyr	Asp	Val	Val	
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ggc	gat	cct	tcc	ttt	gga	aag	gga	acc	gtc	cag	cag	gcg	gtg	ccg	atg	1544
Gly	Asp	Pro	Ser	Phe	Gly	Lys	Gly	Thr	Val	Gln	Gln	Ala	Val	Pro	Met	
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gga	gac	ggt	agc	aat	att	aag	ctg	acg	ctg	tac	aaa	tgg	ctg	aca	cct	1592
Gly	Asp	Gly	Ser	Asn	Ile	Lys	Leu	Thr	Leu	Tyr	Lys	Trp	Leu	Thr	Pro	
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 acg cag cct gca tat ttc tcg gcg ggg cct tta cag ctg aaa gaa ccc 1688
 Thr Gln Pro Ala Tyr Phe Ser Ala Gly Pro Leu Gln Leu Lys Glu Pro 390
 375 380
 ctc aag ccg gat atg aac aac aat gaa att aag cgg gcg cag ttc ctg 1736
 Leu Lys Pro Asp Met Asn Asn Asn Glu Ile Lys Arg Ala Gln Phe Leu 405
 395 400
 ctg aaa gga ctc ggg ttt gtc ccc ggc cgg gaa gac ggc tat tac aat 1784
 Leu Lys Gly Leu Gly Phe Val Pro Gly Arg Glu Asp Gly Tyr Tyr Asn 420
 410 415
 gaa agc aca aaa aaa gcc gtc atg gcg ttt cag gca gca aac aag ctg 1832
 Glu Ser Thr Lys Lys Ala Val Met Ala Phe Gln Ala Ala Asn Lys Leu 435
 425 430
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 Lys Gln Thr Gly Ile Ile Asp Gln Lys Thr Ala Asn Thr Met Asn Leu 450
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 Arg Ile Glu Glu Lys Lys Met Asp Glu Lys Asn Asp Leu Gln Leu Gln 470
 455 460 465
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 Ala Ala Leu Lys Val Leu Phe Asn Lys Lys 480
 475 480
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<213> Bacillus licheniformis

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Ser Lys Ala Ser Ala Ala Glu Glu Ala Ala Ala Lys Ser Thr Ala Arg
 35 40 45

Asn Glu Leu Glu Lys Ile Glu Lys Ala Tyr Asp Leu Ile Ser Asn Glu
 50 55 60

Tyr Val Glu Gln Val Asp Arg Glu Lys Leu Leu Glu Gly Ala Ile Gln
 65 70 75 80

Gly Met Leu Ser Thr Leu Asn Asp Pro Tyr Ser Val Tyr Met Asp Lys
 85 90 95

Gln Thr Ala Lys Arg Phe Ser Asp Ser Leu Asp Ser Ser Phe Glu Gly
 100 105 110

Ile Gly Ala Glu Ile Gly Met Glu Asp Arg Lys Ile Ile Ile Val Ser
 115 120 125

Pro Phe Lys Gln Ser Pro Ala Glu Lys Ala Gly Leu Lys Pro Asn Asp
 130 135 140

Glu Ile Ile Ser Ile Asp Gly Asp Ser Met Ser Gly Met Asp Leu Asn
 145 150 155 160

Asp Ala Val Leu Lys Ile Arg Gly Lys Lys Gly Ser Thr Val Thr Leu
 165 170 175

Lys Val His Arg Pro Gly Met Lys Asp Gln Leu Thr Phe Thr Ile Lys
 180 185 190

Arg Asp Glu Ile Pro Leu Glu Thr Val Phe Ala Ser Ile Lys Lys Val
 195 200 205

Gln Asp Lys Pro Val Gly Tyr Ile Ala Ile Ser Ser Phe Ser Glu His
 210 215 220

Thr Ala Lys Asp Phe Thr Ala Glu Leu Lys Lys Leu Glu Lys Lys Gly
 225 230 235 240

Ile Lys Gly Leu Val Leu Asp Val Arg Gly Asn Pro Gly Gly Tyr Leu
 245 250 255

Gln Ser Val Glu Asp Ile Leu Lys His Phe Val Thr Lys Asp His Pro
 260 265 270

Tyr Ile Gln Ile Ala Glu Arg Asn Gly Asn Lys Lys Gln Tyr Phe Ser
 275 280 285

Lys Leu Lys Glu Lys Lys Pro Tyr Pro Val Ser Val Ile Thr Asp Lys
 290 295 300

Gly Ser Ala Ser Ala Ser Glu Ile Leu Ala Gly Ala Leu Lys Glu Ala
 305 310 315 320

Glu Gly Tyr Asp Val Val Gly Asp Pro Ser Phe Gly Lys Gly Thr Val
 325 330 335

Gln Gln Ala Val Pro Met Gly Asp Gly Ser Asn Ile Lys Leu Thr Leu
 340 345 350

Tyr Lys Trp Leu Thr Pro Lys Gly Asn Trp Ile His Lys Gln Gly Ile
 355 360 365

Gln Pro Thr Val Pro Val Thr Gln Pro Ala Tyr Phe Ser Ala Gly Pro
 370 375 380

Leu Gln Leu Lys Glu Pro Leu Lys Pro Asp Met Asn Asn Asn Glu Ile
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Lys Arg Ala Gln Phe Leu Leu Lys Gly Leu Gly Phe Val Pro Gly Arg
 405 410 415

Glu Asp Gly Tyr Tyr Asn Glu Ser Thr Lys Lys Ala Val Met Ala Phe
 420 425 430

Gln Ala Ala Asn Lys Leu Lys Gln Thr Gly Ile Ile Asp Gln Lys Thr
 435 440 445

Ala Asn Thr Met Asn Leu Arg Ile Glu Glu Lys Lys Met Asp Glu Lys
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<211> 2542

<212> DNA

<213> Bacillus licheniformis

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<222> (977)..(2383)

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Met Ala Lys Gln Gln Ile Gly Val Val Gly Leu Ala	
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gta atg gga aaa aac ttg gct tta aac att gaa agc cgc ggg ttt tca	1060
Val Met Gly Lys Asn Leu Ala Leu Asn Ile Glu Ser Arg Gly Phe Ser	
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gtt tct gtc tac aac aga tca agc gag aaa acc gaa gag ttt ctg aaa	1108
Val Ser Val Tyr Asn Arg Ser Ser Glu Lys Thr Glu Glu Phe Leu Lys	
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gaa gcc gaa ggc aaa aac gtt gtc ggt aca tac agc att gaa gag ttt	1156
Glu Ala Glu Gly Lys Asn Val Val Gly Thr Tyr Ser Ile Glu Glu Phe	
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gtt gaa tct ctt gaa aaa ccg cgc aaa att ctt tta atg gtc aaa gct	1204
Val Glu Ser Leu Glu Lys Pro Arg Lys Ile Leu Leu Met Val Lys Ala	
65 70 75	
gga aca ccg aca gac gca acg att caa tcg ctt ctg cct cat ctt gaa	1252
Gly Thr Pro Thr Asp Ala Thr Ile Gln Ser Leu Leu Pro His Leu Glu	
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aaa ggc gac att ttg att gac ggc gga aat aca tat tat aaa gat acg	1300
Lys Gly Asp Ile Leu Ile Asp Gly Gly Asn Thr Tyr Tyr Lys Asp Thr	
95 100 105	
cag aga aga aac agg gag ctg gcc gaa agc ggc att cac ttc atc ggc	1348
Gln Arg Arg Asn Arg Glu Leu Ala Glu Ser Gly Ile His Phe Ile Gly	
110 115 120	
acc ggc gtt tcc ggc ggt gaa gaa ggc gct ctg aaa ggg ccg tct atc	1396
Thr Gly Val Ser Gly Gly Glu Glu Gly Ala Leu Lys Gly Pro Ser Ile	
125 130 135 140	
atg cca ggc gga caa aag gaa gcc cat gag ctt gtc aag ccg att ctt	1444
Met Pro Gly Gly Gln Lys Glu Ala His Glu Leu Val Lys Pro Ile Leu	
145 150 155	

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gaa tac ggc gat atg cag ctg atc tca gaa tcc tac ttt att ttg aaa Glu Tyr 190 Gly Asp Met Gln 195 Leu Ile Ser Glu Ser 200 Tyr Phe Ile Leu Lys	1588
cac att gtc ggt ctg tca tca gat gag ctt cac gaa gtc ttt tcc gag His Ile Val Gly Leu 210 Ser Ser Asp Glu Leu 215 His Glu Val Phe Ser 220 Glu	1636
tgg aat aag gga gag ctt gac agc tat ctg atc gaa atc acg gct gat Trp Asn Lys Gly 225 Glu Leu Asp Ser Tyr 230 Leu Ile Glu Ile Thr 235 Ala Asp	1684
att ttc acg aaa aaa gac gag gaa acc ggc aag ccg ctt gtt gac gtc Ile Phe Thr Lys 240 Lys Asp Glu Glu 245 Thr Gly Lys Pro Leu Val 250 Asp Val	1732
atc ctc gat aaa gca ggt caa aaa ggc aca gga aaa tgg aca agc caa Ile Leu Asp 255 Lys Ala Gly Gln 260 Lys Gly Thr Gly Lys Trp 265 Thr Ser Gln	1780
agc gct ctt gac ctg ggc gtt ccg ctt cca atc att acg gaa tct gtt Ser Ala 270 Leu Asp Leu Gly 275 Val Pro Leu Pro Ile 280 Thr Glu Ser Val	1828
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gag ctg atc gaa gcg gtc aga aaa gcg ctc ttc atg agc aaa atc tgt Glu Leu Ile 320 Glu Ala Val Arg Lys Ala 325 Leu Phe Met Ser Lys 330 Ile Cys	1972
tct tac gcc caa ggc ttt gct caa atg aaa gcc gca tca gaa gaa tac Ser Tyr 335 Ala Gln Gly Phe Ala Gln Met Lys Ala Ala Ser 345 Glu Glu Tyr	2020
ggc tgg gat ttg aaa tac ggc gat atc gcg atg att ttc cgc gga gga Gly Trp 350 Asp Leu Lys Tyr 355 Gly Asp Ile Ala Met 360 Ile Phe Arg Gly Gly	2068
tgc atc atc cgc gcg gcg ttc ctg caa aaa atc aaa gaa gcg tat gac Cys Ile 365 Ile Arg Ala Ala 370 Phe Leu Gln Lys Ile 375 Lys Glu Ala Tyr Asp 380	2116
cgc gat cca gag ctt gac aac ctg ctt ctt gac ccg tac ttc aaa aat Arg Asp 385 Pro Glu Leu Asp Asn Leu Leu 390 Asp Pro Tyr Phe Lys 395 Asn	2164
atc gtt gaa agc tat cag gga gcc ctc cgc aaa acg att tct ctt gcg Ile Val 400 Glu Ser Tyr Gln Gly Ala Leu 405 Arg Lys Thr Ile Ser Leu Ala	2212
gtt gaa caa gga att cct gta cct tgc ttc tca agc gct ctc gct tac Val Glu 415 Gln Gly Ile Pro Val 420 Pro Cys Phe Ser Ser 425 Ala Leu Ala Tyr	2260

10294.000.ST25.txt

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ttt gac agc tac cgc act gca acc ctg ccg gcc aac ctg att cag gcg      2308
Phe Asp Ser Tyr Arg Thr Ala Thr Leu Pro Ala Asn Leu Ile Gln Ala
430          435          440

cag cgc gac tac ttt ggc gcc cat acg tat gag cgt aca gat aaa gaa      2356
Gln Arg Asp Tyr Phe Gly Ala His Thr Tyr Glu Arg Thr Asp Lys Glu
445          450          455          460

ggc att ttc cac act gag tgg atg aaa taagatgtaa aaccgcaagc      2403
Gly Ile Phe His Thr Glu Trp Met Lys
465

tgaaaagctt gcggtttttt tgattttcgg aaggatgcat gtttaagcgg ttgtgtggaa      2463

acctactcaa aagtgagttt caataaggag gaatcaaccc atgtatccaa gtttagaggg      2523

aaaaacggtc gttatcaca      2542

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<210> 14

<211> 469

<212> PRT

<213> Bacillus licheniformis

<400> 14

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Asn Leu Ala Leu Asn Ile Glu Ser Arg Gly Phe Ser Val Ser Val Tyr
20          25          30

Asn Arg Ser Ser Glu Lys Thr Glu Glu Phe Leu Lys Glu Ala Glu Gly
35          40          45

Lys Asn Val Val Gly Thr Tyr Ser Ile Glu Glu Phe Val Glu Ser Leu
50          55          60

Glu Lys Pro Arg Lys Ile Leu Leu Met Val Lys Ala Gly Thr Pro Thr
65          70          75          80

Asp Ala Thr Ile Gln Ser Leu Leu Pro His Leu Glu Lys Gly Asp Ile
85          90          95

Leu Ile Asp Gly Gly Asn Thr Tyr Tyr Lys Asp Thr Gln Arg Arg Asn
100          105          110

Arg Glu Leu Ala Glu Ser Gly Ile His Phe Ile Gly Thr Gly Val Ser
115          120          125

Gly Gly Glu Glu Gly Ala Leu Lys Gly Pro Ser Ile Met Pro Gly Gly
130          135          140

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Gln Lys Glu Ala His Glu Leu Val Lys Pro Ile Leu Glu Ala Ile Ser
 145 150 155 160

Ala Lys Val Asp Gly Glu Pro Cys Thr Thr Tyr Ile Gly Pro Asp Gly
 165 170 175

Ala Gly His Tyr Val Lys Met Val His Asn Gly Ile Glu Tyr Gly Asp
 180 185 190

Met Gln Leu Ile Ser Glu Ser Tyr Phe Ile Leu Lys His Ile Val Gly
 195 200 205

Leu Ser Ser Asp Glu Leu His Glu Val Phe Ser Glu Trp Asn Lys Gly
 210 215 220

Glu Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Asp Ile Phe Thr Lys
 225 230 235 240

Lys Asp Glu Glu Thr Gly Lys Pro Leu Val Asp Val Ile Leu Asp Lys
 245 250 255

Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ser Gln Ser Ala Leu Asp
 260 265 270

Leu Gly Val Pro Leu Pro Ile Ile Thr Glu Ser Val Phe Ala Arg Phe
 275 280 285

Ile Ser Ser Met Lys Glu Glu Arg Val Lys Ala Ser Lys Leu Leu Ala
 290 295 300

Gly Pro Glu Ala Lys Pro Ala Ala Glu Asn Lys Glu Glu Leu Ile Glu
 305 310 315 320

Ala Val Arg Lys Ala Leu Phe Met Ser Lys Ile Cys Ser Tyr Ala Gln
 325 330 335

Gly Phe Ala Gln Met Lys Ala Ala Ser Glu Glu Tyr Gly Trp Asp Leu
 340 345 350

Lys Tyr Gly Asp Ile Ala Met Ile Phe Arg Gly Gly Cys Ile Ile Arg
 355 360 365

Ala Ala Phe Leu Gln Lys Ile Lys Glu Ala Tyr Asp Arg Asp Pro Glu
 370 375 380

Leu Asp Asn Leu Leu Leu Asp Pro Tyr Phe Lys Asn Ile Val Glu Ser
 385 390 395 400

Tyr Gln Gly Ala Leu Arg Lys Thr Ile Ser Leu Ala Val Glu Gln Gly
 405 410 415

Ile Pro Val Pro Cys Phe Ser Ser Ala Leu Ala Tyr Phe Asp Ser Tyr
 420 425 430

Arg Thr Ala Thr Leu Pro Ala Asn Leu Ile Gln Ala Gln Arg Asp Tyr
 435 440 445

Phe Gly Ala His Thr Tyr Glu Arg Thr Asp Lys Glu Gly Ile Phe His
 450 455 460

Thr Glu Trp Met Lys
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<210> 15

<211> 2030

<212> DNA

<213> Bacillus Ticheniformis

<220>

<221> CDS

<222> (501)..(1391)

<223>

<400> 15

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tcgcggaaaa acataatgtc gacatcgccc atatcgtctt ggcctggtac ttggcgcggc 120

ctgaaatcga cgtgttgatc ccgggcgcca aacgcgctga tcagctgac gacaacctca 180

aaacggcaga agtcaatctg tctcaagagg acattgattt catcgaccgg ctgtttgccc 240

gctaaatgat caggaaacct atcttaaaag ataggtttct ttatttttaa aatcctgttg 300

acagcgcttc cttttttgat atgataggaa agaagttaat acaagtgacg gagaatggga 360

gattcacaat aagaccctct tgtgccaggg gtttttttgt ggatctcttt ttcttcgtca 420

tctaagaggg ggcgaaagca atcgtaatga atagacggca cttttattct gtataacagc 480

ttgaaaggag agatcatgtt atg aaa aga cta gtc cgc agc atc ttc ctt ata 533
 Met Lys Arg Leu Val Arg Ser Ile Phe Leu Ile
 1 5 10

acg gcc gca atc gct gct ttt ggt ttt gga ttc agc ggg cat gcg gag 581
 Thr Ala Ala Ile Ala Ala Phe Gly Phe Gly Phe Ser Gly His Ala Glu
 15 20 25

gcg gca agc cat tcc cag ccg cag ctc aat ccg aac aag cta cta aat 629
 Ala Ala Ser His Ser Gln Pro Gln Leu Asn Pro Asn Lys Leu Leu Asn
 30 35 40

gtc gcg cac cgc ggc gca tcg ggg cat gct ccc gag cac acg ctt ttg 677
 Val Ala His Arg Gly Ala Ser Gly His Ala Pro Glu His Thr Leu Leu
 45 50 55

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gct tat aag ctt gga caa aaa atg aaa ggc gat tac ata gaa atc gat Ala Tyr Lys Leu Gly Gln Lys Met Lys Gly Asp Tyr Ile Glu Ile Asp 60 65 70 75	725
ctt caa atg aca aaa gac ggc cac ttg gtc gcc atg cac gat gag aca Leu Gln Met Thr Lys Asp Gly His Leu Val Ala Met His Asp Glu Thr 80 85 90	773
ttg gat cgt acg act aat ggt acg ggt ttt gtc aaa gac tat acg ctg Leu Asp Arg Thr Thr Asn Gly Thr Gly Phe Val Lys Asp Tyr Thr Leu 95 100 105	821
aaa gaa atc aaa gag ctt gat gca ggc tcc tgg ttt aac gaa gca tat Lys Glu Ile Lys Glu Leu Asp Ala Gly Ser Trp Phe Asn Glu Ala Tyr 110 115 120	869
cct gag cgg gca aaa ccg gag tac gcc ggg ctg aaa gtg ccc acc ctt Pro Glu Arg Ala Lys Pro Glu Tyr Ala Gly Leu Lys Val Pro Thr Leu 125 130 135	917
gaa gaa atc atc caa aca ttc ggg aga agc gcg cgc tac tat atc gaa Glu Glu Ile Ile Gln Thr Phe Gly Arg Ser Ala Arg Tyr Tyr Ile Glu 140 145 150 155	965
aca aaa tca ccg gaa gac tat gat cat atg gaa gaa aag ctc ctg gac Thr Lys Ser Pro Glu Asp Tyr Asp His Met Glu Glu Lys Leu Leu Asp 160 165 170	1013
atc ctg aag caa tac aaa ttg acc gga gca gac att cat tca agc aaa Ile Leu Lys Gln Tyr Lys Leu Thr Gly Ala Asp Ile His Ser Ser Lys 175 180 185	1061
gtc atc att caa tct ttt agt cct gaa agc tta aaa atc att cat aac Val Ile Ile Gln Ser Phe Ser Pro Glu Ser Leu Lys Ile Ile His Asn 190 195 200	1109
gct aat cca aac att ccg cta gtg caa tta tta tgg tac gac aaa cct Ala Asn Pro Asn Ile Pro Leu Val Gln Leu Leu Trp Tyr Asp Lys Pro 205 210 215	1157
gct gcc att act gac gcc gaa tta aaa caa tat caa tct tac agc gtc Ala Ala Ile Thr Asp Ala Glu Leu Lys Gln Tyr Gln Ser Tyr Ser Val 220 225 230 235	1205
gga ctc ggc atg aac ttt gac cgc att ggc cgg gca tac gtg caa aag Gly Leu Gly Met Asn Phe Asp Arg Ile Gly Arg Ala Tyr Val Gln Lys 240 245 250	1253
att cga cgc acc ggc atg ctg gtc cat cct tat act gtg aat aaa aaa Ile Arg Arg Thr Gly Met Leu Val His Pro Tyr Thr Val Asn Lys Lys 255 260 265	1301
gaa gat atg aag cgg ctg ctc gat tgg gga gcg acc gga atg ttc acc Glu Asp Met Lys Arg Leu Leu Asp Trp Gly Ala Thr Gly Met Phe Thr 270 275 280	1349
aac ttt ccg gac cgg ctg cgc gat gtt ttg cgc gaa aag aag Asn Phe Pro Asp Arg Leu Arg Asp Val Leu Arg Glu Lys Lys 285 290 295	1391
taaataaata aagaagggga ataccatgtt aaaactgttt aagccagcac cgccgattga	1451
gcggctgccg gaagatcaaa ttgattcgga atataagaaa ttcagactgc aagtttttct	1511
cggcattctt atcgggttatg cggcatacta tttaattcgc aaaaatttct cgcttgccat	1571
gccttatttg atcgaagagg gcttttcaaa gtcggcgctc ggctttgcct tgtccgctct	1631

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gaggatgttc ctgcccgccg gtttgatcct ttccgtgtc atcagcctct tgatggggtt 1751
tgttcctttt ttcacctcat cgatcgccat tatgtttatc atgctgttct taaacggctg 1811
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<210> 16

<211> 297

<212> PRT

<213> Bacillus licheniformis

<400> 16

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Ala Phe Gly Phe Gly Phe Ser Gly His Ala Glu Ala Ala Ser His Ser
20 25 30

Gln Pro Gln Leu Asn Pro Asn Lys Leu Leu Asn Val Ala His Arg Gly
35 40 45

Ala Ser Gly His Ala Pro Glu His Thr Leu Leu Ala Tyr Lys Leu Gly
50 55 60

Gln Lys Met Lys Gly Asp Tyr Ile Glu Ile Asp Leu Gln Met Thr Lys
65 70 75 80

Asp Gly His Leu Val Ala Met His Asp Glu Thr Leu Asp Arg Thr Thr
85 90 95

Asn Gly Thr Gly Phe Val Lys Asp Tyr Thr Leu Lys Glu Ile Lys Glu
100 105 110

Leu Asp Ala Gly Ser Trp Phe Asn Glu Ala Tyr Pro Glu Arg Ala Lys
115 120 125

Pro Glu Tyr Ala Gly Leu Lys Val Pro Thr Leu Glu Glu Ile Ile Gln
130 135 140

Thr Phe Gly Arg Ser Ala Arg Tyr Tyr Ile Glu Thr Lys Ser Pro Glu
145 150 155 160

Asp Tyr Asp His Met Glu Glu Lys Leu Leu Asp Ile Leu Lys Gln Tyr
 165 170 175

Lys Leu Thr Gly Ala Asp Ile His Ser Ser Lys Val Ile Ile Gln Ser
 180 185 190

Phe Ser Pro Glu Ser Leu Lys Ile Ile His Asn Ala Asn Pro Asn Ile
 195 200 205

Pro Leu Val Gln Leu Leu Trp Tyr Asp Lys Pro Ala Ala Ile Thr Asp
 210 215 220

Ala Glu Leu Lys Gln Tyr Gln Ser Tyr Ser Val Gly Leu Gly Met Asn
 225 230 235 240

Phe Asp Arg Ile Gly Arg Ala Tyr Val Gln Lys Ile Arg Arg Thr Gly
 245 250 255

Met Leu Val His Pro Tyr Thr Val Asn Lys Lys Glu Asp Met Lys Arg
 260 265 270

Leu Leu Asp Trp Gly Ala Thr Gly Met Phe Thr Asn Phe Pro Asp Arg
 275 280 285

Leu Arg Asp Val Leu Arg Glu Lys Lys
 290 295

<210> 17

<211> 2308

<212> DNA

<213> Bacillus licheniformis

<220>

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<222> (501)..(1814)

<223>

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aacgggggatc cttttgaatg caaagggtcag ctctgagcta ttgatcaaca tctttattcc	180
gaacactccg cttcatgacg gagccgtgat tatgaaaaac gatgagggtg ctgcagctgc	240
ctgctacctt ccgctttctg aaagcccttt tatttcaaaa gagcttggaa cgaggcacag	300
agcagcagtg ggaatcagtg aagtgaccga cagtctgacg gttgttgat ccgaagagac	360

10294.000.ST25.txt

gggcggcatc agcgtcgcca aaaacggaga ccttcaccgt gatttatcgg aagaggcatt 420
gaaaaatatg cttgaagcgg aattttaagaa aaattcgcgg gaaacttcct caaatcgctg 480
gtattggagg gcgaagaaaa atg gat aag ttc tta aac aat ccc tgg gct gtc 533
Met Asp Lys Phe Leu Asn Asn Pro Trp Ala Val
1 5 10
aaa gtt gtc gcg tta ttg ttc gcg ttt ctt ctt tac ttt gcg gtc cac 581
Lys Val Val Ala Leu Leu Phe Ala Phe Leu Leu Tyr Phe Ala Val His
15 20 25
agc gct cag gcg ccg act ccg aag aaa cca ggt gaa tcg ttt ttc ccg 629
Ser Ala Gln Ala Pro Thr Pro Lys Lys Pro Gly Glu Ser Phe Phe Pro
30 35 40
aca tcg aca aca gac gaa gcg acg ctc acc gat ata ccg gtc aaa tcg 677
Thr Ser Thr Thr Asp Glu Ala Thr Leu Thr Asp Ile Pro Val Lys Ser
45 50 55
ttt tat gat gat gaa aac tac gtc gta aca ggc gtg ccg cag acg gtg 725
Phe Tyr Asp Asp Glu Asn Tyr Val Val Thr Gly Val Pro Gln Thr Val
60 65 70 75
aat gtc acg att aaa ggc ccg acc gga acc gtc aag aag gtc aga caa 773
Asn Val Thr Ile Lys Gly Pro Thr Gly Thr Val Lys Lys Val Arg Gln
80 85 90
gtg aag gat ttt gag att tat gcc gac atg caa aac ctg aaa aca ggc 821
Val Lys Asp Phe Glu Ile Tyr Ala Asp Met Gln Asn Leu Lys Thr Gly
95 100 105
agg cat aaa gtc gag ctg aag gcc aga aat gtt gcc gac ggc ctc act 869
Arg His Lys Val Glu Leu Lys Ala Arg Asn Val Ala Asp Gly Leu Thr
110 115 120
ctg acc atc aat cca tcg gtg aca acc gtg acg atc gaa gaa aaa acg 917
Leu Thr Ile Asn Pro Ser Val Thr Thr Val Thr Ile Glu Glu Lys Thr
125 130 135
acg aag gaa ttc ccg gtc gag gtt gat ttt tat aat aaa aac aaa atg 965
Thr Lys Glu Phe Pro Val Glu Val Asp Phe Tyr Asn Lys Asn Lys Met
140 145 150 155
aaa gac ggc tac acg ccg gag ctg ccg atc atc aac ccg aaa aac gtc 1013
Lys Asp Gly Tyr Thr Pro Glu Leu Pro Ile Ile Asn Pro Lys Asn Val
160 165 170
agc gtc acc ggc tca aaa gcc gtg atc gac aga atc cag aac atc aag 1061
Ser Val Thr Gly Ser Lys Ala Val Ile Asp Arg Ile Gln Asn Ile Lys
175 180 185
gcg acg atc aat tta gag ggc gtc gac cag acg gtt gaa aaa gaa gcc 1109
Ala Thr Ile Asn Leu Glu Gly Val Asp Gln Thr Val Glu Lys Glu Ala
190 195 200
aag ctt aca gta tac gac aag gac gga aat gtc ctg ccg gtt gaa gtc 1157
Lys Leu Thr Val Tyr Asp Lys Asp Gly Asn Val Leu Pro Val Glu Val
205 210 215
agc cct tcc gtc gtt aaa atc acc gtt ccg gtg acg agc ccg agc aaa 1205
Ser Pro Ser Val Val Lys Ile Thr Val Pro Val Thr Ser Pro Ser Lys
220 225 230 235
aag att ccg gtc aaa gtt gac cgg aaa ggc agc ctt ccg gac ggc atc 1253
Lys Ile Pro Val Lys Val Asp Arg Lys Gly Ser Leu Pro Asp Gly Ile
240 245 250

10294.000.ST25.txt

agc att tcc agc ctc gat ata agt ccg gga gag gtg acc gtc tac ggg Ser Ile Ser Ser Leu Asp Ile Ser Pro Gly Glu Val Thr Val Tyr Gly	1301
ccg caa aat gtt ctt gat tcg tta gaa ttt gtc gag gcc gac gag att Pro Gln Asn Val Leu Asp Ser Leu Glu Phe Val Glu Ala Asp Glu Ile	1349
gat tta agt aaa ata aag gat gat act gaa ttg gaa gcc ggc att aaa Asp Leu Ser Lys Ile Lys Asp Asp Thr Glu Leu Glu Ala Gly Ile Lys	1397
gtg ccg gac ggc gct aaa aag gtg tca ccc gaa aaa gtg aaa atc aag Val Pro Asp Gly Ala Lys Lys Val Ser Pro Glu Lys Val Lys Ile Lys	1445
gtg aaa gtt gac aag gaa gaa gag aaa aaa ctg aaa aac gtt tca att Val Lys Val Asp Lys Glu Glu Glu Lys Lys Leu Lys Asn Val Ser Ile	1493
aaa acc gcg ggc ctg aat gac agc cgg gat ctt gaa ttt ctc gat ccg Lys Thr Ala Gly Leu Asn Asp Ser Arg Asp Leu Glu Phe Leu Asp Pro	1541
aag tca ggc aag ctg gat atc acg gca aag ggc tcg aca gcc gcg atc Lys Ser Gly Lys Leu Asp Ile Thr Ala Lys Gly Ser Thr Ala Ala Ile	1589
gaa aaa ctc cag cct tcc gac gtc gag ctc tat gtc aat gtg gcg gat Glu Lys Leu Gln Pro Ser Asp Val Glu Leu Tyr Val Asn Val Ala Asp	1637
ctc gat gac ggc gag cac aat gta aag ctg gaa gta aac ggt ccg cag Leu Asp Asp Gly Glu His Asn Val Lys Leu Glu Val Asn Gly Pro Gln	1685
aac atg aca tgg tcg ctg ccg cgg caa agc att cga gtg aaa atc tca Asn Met Thr Trp Ser Leu Pro Arg Gln Ser Ile Arg Val Lys Ile Ser	1733
tct caa aca acc caa aac gaa aaa aac aat ggt cag gat gaa gaa gaa Ser Gln Thr Thr Gln Asn Glu Lys Asn Asn Gly Gln Asp Glu Glu Glu	1781
gag aat cat tct gaa aag gat tca caa cct tca tgaatcaaaa aggagcgata Glu Asn His Ser Glu Lys Asp Ser Gln Pro Ser	1834
ttaatgggca agtatttttg tacagacggt gtaagaggcg tggcaaacag tgaacttaca	1894
cctgagctgg cttttaaagt cggacgcttt ggcggatatg tcctaacaaa agataaggag	1954
cgtcccaagg ttctgatcgg ccgtgacacg cgcatttcag ggcatatgct ggaagggggcc	2014
cttgtagcag gccttctttc gataggagca gaagtcatgc gtctcggcgt gatttcgacg	2074
cccggagtcg catatttgac gaaggctatg gacgcggagg cgggtgtgat gatttccgct	2134
tcccacaacc ctgtccagga caacggaatt aagtttttcg gcggcgacgg ctttaagctt	2194
tccgatgaac aggagcttga aatcgagcgt ctgatggatc agccggaaga tcacctgcca	2254
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<211> 438

<212> PRT

<213> Bacillus Ticheniformis

<400> 18

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Thr Pro Lys Lys Pro Gly Glu Ser Phe Phe Pro Thr Ser Thr Thr Asp
 35 40 45

Glu Ala Thr Leu Thr Asp Ile Pro Val Lys Ser Phe Tyr Asp Asp Glu
 50 55 60

Asn Tyr Val Val Thr Gly Val Pro Gln Thr Val Asn Val Thr Ile Lys
 65 70 75 80

Gly Pro Thr Gly Thr Val Lys Lys Val Arg Gln Val Lys Asp Phe Glu
 85 90 95

Ile Tyr Ala Asp Met Gln Asn Leu Lys Thr Gly Arg His Lys Val Glu
 100 105 110

Leu Lys Ala Arg Asn Val Ala Asp Gly Leu Thr Leu Thr Ile Asn Pro
 115 120 125

Ser Val Thr Thr Val Thr Ile Glu Glu Lys Thr Thr Lys Glu Phe Pro
 130 135 140

Val Glu Val Asp Phe Tyr Asn Lys Asn Lys Met Lys Asp Gly Tyr Thr
 145 150 155 160

Pro Glu Leu Pro Ile Ile Asn Pro Lys Asn Val Ser Val Thr Gly Ser
 165 170 175

Lys Ala Val Ile Asp Arg Ile Gln Asn Ile Lys Ala Thr Ile Asn Leu
 180 185 190

Glu Gly Val Asp Gln Thr Val Glu Lys Glu Ala Lys Leu Thr Val Tyr
 195 200 205

Asp Lys Asp Gly Asn Val Leu Pro Val Glu Val Ser Pro Ser Val Val
 210 215 220

Lys Ile Thr Val Pro Val Thr Ser Pro Ser Lys Lys Ile Pro Val Lys
 225 230 235 240

Val Asp Arg Lys Gly Ser Leu Pro Asp Gly Ile Ser Ile Ser Ser Leu
245 250 255

Asp Ile Ser Pro Gly Glu Val Thr Val Tyr Gly Pro Gln Asn Val Leu
260 265 270

Asp Ser Leu Glu Phe Val Glu Ala Asp Glu Ile Asp Leu Ser Lys Ile
275 280 285

Lys Asp Asp Thr Glu Leu Glu Ala Gly Ile Lys Val Pro Asp Gly Ala
290 295 300

Lys Lys Val Ser Pro Glu Lys Val Lys Ile Lys Val Lys Val Asp Lys
305 310 315 320

Glu Glu Glu Lys Lys Leu Lys Asn Val Ser Ile Lys Thr Ala Gly Leu
325 330 335

Asn Asp Ser Arg Asp Leu Glu Phe Leu Asp Pro Lys Ser Gly Lys Leu
340 345 350

Asp Ile Thr Ala Lys Gly Ser Thr Ala Ala Ile Glu Lys Leu Gln Pro
355 360 365

Ser Asp Val Glu Leu Tyr Val Asn Val Ala Asp Leu Asp Asp Gly Glu
370 375 380

His Asn Val Lys Leu Glu Val Asn Gly Pro Gln Asn Met Thr Trp Ser
385 390 395 400

Leu Pro Arg Gln Ser Ile Arg Val Lys Ile Ser Ser Gln Thr Thr Gln
405 410 415

Asn Glu Lys Asn Asn Gly Gln Asp Glu Glu Glu Glu Asn His Ser Glu
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Lys Asp Ser Gln Pro Ser
435

<210> 19

<211> 2632

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (852)..(2606)

<223>

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cggcaagcgt ttttccccgt gtaaccggga cccttctgat ctgataatct cccatgagat      180
cgaccgcttt tcaatgaatg tttacactta ccgtaatgat agaagggccc tttggatatg      240
aacgattcat cgaagcgatc ccgtcttata aagaagtgtt tggcacagac gaaaagggtgt      300
ggacaaaagc atcgccgctc tcatacataa acaactcaaa attgccgccg gcctatcttg      360
tgacccgctg ggaagaccct gccgtttaca agttcgcgga aaccgcaaac aaagcgaagg      420
caacggaatt tgtgtatcaa gtcaacagct tatctcacag tgatttaaac aagatgttcg      480
gctctccaga tgcaccggca gaagcgcaga atctgacaaa agcgggttatg gcgttttttag      540
agaaggaaaa taaatagatc aaacggccga ctcggcttcc tacatgtact tgctgaaagg      600
atataaacag ctgttaaact agcagagaaa ggccgaaaat gttaaattcg gcctcttctc      660
acacttggca ccccttact cataagacat cgatctgaaa attcccaaaa tataaacaaa      720
acattaataa aatcaagcca tttgattaac aaatttacga tacgatcata tagaacttga      780
tgattgggaa aagcattttg agagaagatt aagagcaagg gagatatgat gtgagaatga      840
aacgattaag g atg agg aag cat tta ctg ata gct gtc tgt act ttg gca      890
          Met Arg Lys His Leu Leu Ile Ala Val Cys Thr Leu Ala
          1          5          10

ctt ctt cta agt tcc ccg att gta agc gat gcg agc ccg gca act aaa      938
Leu Leu Leu Ser Ser Pro Ile Val Ser Asp Ala Ser Pro Ala Thr Lys
          15          20          25

cca aca act gca gat tcg ccg caa tct tcc gga ttt ttc gta gac cat      986
Pro Thr Thr Ala Asp Ser Pro Gln Ser Ser Gly Phe Phe Val Asp His
          30          35          40          45

tac aaa aat aat atc tct gcc aat acg acg gcg gaa tcc aat cct gtc      1034
Tyr Lys Asn Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn Pro Val
          50          55          60

atc ggc ctg ctt tcc gaa ttt aat aaa ctt tgg act ccc gga aag aca      1082
Ile Gly Leu Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly Lys Thr
          65          70          75

tgg aat acc ggt act aaa ctg aac agc agg gtg ctg gat gcc aac att      1130
Trp Asn Thr Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala Asn Ile
          80          85          90

caa aaa gtc gtg gat att gct gaa cgc cgc acg atg ctt gag gaa aat      1178
Gln Lys Val Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu Glu Asn
          95          100          105

gct gcc tat ttt gat gat cgg cgg agc cag agc tac agt ata att gac      1226
Ala Ala Tyr Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile Ile Asp
          110          115          120          125

ggc ctc ggc aag ctt gcc ggc gtc tat cga atg aac gcg gga gcg acg      1274

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10294.000.ST25.txt

Gly	Leu	Gly	Lys	Leu	Ala	Gly	Val	Tyr	Arg	Met	Asn	Ala	Gly	Ala	Thr	
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Val	Ser	Leu	Val	Asn	Thr	Leu	Arg	Gly	Asn	Tyr	Ser	Ser	Ser	Asn	Pro	
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Ser	Ile	Ile	Val	Pro	Thr	Leu	Ile	Pro	Val	Ile	Asn	Pro	Asp	Pro	Asn	
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Lys	Asp	Gly	Gly	Phe	Pro	Ser	Gly	His	Thr	Asn	Ala	Ala	Tyr	Leu	Ser	
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Thr	Arg	Ala	Ser	Glu	Leu	Gly	His	Asn	Arg	Ile	Val	Ala	Gly	Met	His	
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Val	Pro	Lys	Gly	Ala	Glu	Val	Leu	Leu	Glu	Thr	Arg	Phe	Pro	Tyr	Leu	
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gac	aaa	aag	cag	cgc	cgt	tcg	gtt	tta	gcc	act	acc	ggt	ctt	ccg	gcc	1994
Asp	Lys	Lys	Gln	Arg	Arg	Ser	Val	Leu	Ala	Thr	Thr	Gly	Leu	Pro	Ala	
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Gly	Tyr	Pro	Val	Leu	Asp	Asp	Arg	Glu	Gly	Trp	Gly	Arg	Leu	Asn	Leu	
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Asp	Gly	Ser	Ala	Ile	Ile	Thr	Phe	Arg	Lys	Arg	His	Gly	Ser	Phe	Ser	
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Ser	Val	Glu	Thr	Ser	Gly	Leu	Pro	Ser	Lys	Tyr	Lys	Val	Lys	Ile	Ile	
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<400> 20

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Ala Asp Ser Pro Gln Ser Ser Gly Phe Phe Val Asp His Tyr Lys Asn
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 Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn Pro Val Ile Gly Leu
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 Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly Lys Thr Trp Asn Thr
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 Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala Asn Ile Gln Lys Val
 85 90 95
 Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu Glu Asn Ala Ala Tyr
 100 105 110
 Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile Ile Asp Gly Leu Gly
 115 120 125
 Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly Ala Thr Thr Thr Ile
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 Thr Ser Ile Pro Ala Asp Ala Ser Ile Arg Lys Tyr Asn Asp Glu Gly
 145 150 155 160
 Thr Asn Ser Gly Ser Thr Ser Ser Glu Leu Gly Asn Val Val Ser Leu
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 Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Ser Asn Pro Ala Lys Ser
 180 185 190
 Tyr Phe Asn Tyr Pro Arg Pro Phe Arg Trp Lys Asp Asn Ser Ile Ile
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 Val Pro Thr Leu Ile Pro Val Ile Asn Pro Asp Pro Asn Lys Asp Gly
 210 215 220
 Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr Leu Ser Ala Phe Ala
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 Ser Glu Leu Gly His Asn Arg Ile Val Ala Gly Met His Ser Pro Leu
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 Asp Val Met Gly Gly Arg Val Met Ala Thr Ala Leu Ser Ala Ala Ile
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 Leu Ser Asp Pro Ala Asn Glu Arg Leu Lys Lys Thr Ala Phe Asp Glu
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 Ala Asp Gly Tyr Gly Ala Phe Thr Lys Asn Val Thr Val Thr Met Asp
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 Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg Trp Arg Asn Asp Ile
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 Leu Glu Gly Gly Ser Glu Thr Ala Phe Gly Arg Gly Asp Val Ala Leu
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 485 490 495
 Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu Glu Leu Gln Leu Ser
 500 505 510
 Gly Lys Lys Asp Gln Leu Lys Ile Lys Gly Lys Ala Arg Leu Lys Gly
 515 520 525
 Thr Leu Arg Leu Asn Phe Thr Asp Asn Tyr Val Pro Ala Asp Gly Ser
 530 535 540
 Ala Ile Ile Thr Phe Arg Lys Arg His Gly Ser Phe Ser Ser Val Glu
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 Thr Ser Gly Leu Pro Ser Lys Tyr Lys Val Lys Ile Ile Tyr Lys Ser
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10294.000.ST25.txt

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Ala	Gln	Asn	Ala	Ser	Ala	Phe	Ser	Gln	Trp	Asn	Ile	Lys	Leu	Ile	Gln	
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gcc	gca	ctg	gct	tgg	aat	aaa	ggt	ttg	acc	gga	aaa	cag	gtg	aag	atc	917
Ala	Ala	Leu	Ala	Trp	Asn	Lys	Gly	Leu	Thr	Gly	Lys	Gln	Val	Lys	Ile	
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gcg	gtt	att	gac	agc	ggg	att	tcc	ccc	cat	gag	gag	ctg	tcg	atc	gcc	965
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Gly	Gly	Ala	Ser	Met	Val	Gly	Tyr	Thr	Ala	Ser	Tyr	Arg	Asp	Asp	Asn	
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ggc	cac	gga	acc	cat	gtt	gcc	gga	atc	atc	gga	gcg	aag	cat	aac	gga	1061
Gly	His	Gly	Thr	His	Val	Ala	Gly	Ile	Ile	Gly	Ala	Lys	His	Asn	Gly	
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cgg	ggg	atc	gac	ggc	atc	gcg	ccc	ggc	gcg	cag	ctg	tat	gcc	gta	aaa	1109
Arg	Gly	Ile	Asp	Gly	Ile	Ala	Pro	Gly	Ala	Gln	Leu	Tyr	Ala	Val	Lys	
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gcg	ctg	gac	cgg	aat	ggt	gcg	ggg	gat	ctg	aaa	ggt	atc	tta	caa	ggc	1157
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Ile	Asp	Trp	Ser	Ile	Gln	His	Gly	Ile	Asp	Ile	Ile	Asn	Met	Ser	Leu	
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gtc	gtt	tca	ggc	gac	agt	caa	gtt	ctc	cac	gat	gcg	gta	gat	aaa	gca	1253
Val	Val	Ser	Gly	Asp	Ser	Gln	Val	Leu	His	Asp	Ala	Val	Asp	Lys	Ala	
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Ser	Ala	Thr	Asn	Glu	Lys	Asn	Gln	Ile	Ala	Ser	Phe	Thr	Asn	Thr	Arg	
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Ser	Ala	Val	Ser	Tyr	Ser	Ala	Pro	Ser	Thr	Ser	Ile	Ile	Asn	Thr	Ser	
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Gly	Asn	Arg	Gly	Tyr	Ala	Ile	Gly	Ser	Cys	Thr	Ala	Gln	Gly	Thr	Pro	
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Ser	Asn	Ala	Glu	Leu	Arg	Lys	Lys	Met	Gln	Phe	Tyr	Thr	Ser	Asp	Leu	
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10294.000.ST25.txt

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Val Gly Tyr Thr Ala Ser Tyr Arg Asp Asp Asn Gly His Gly Thr His
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Val Ala Gly Ile Ile Gly Ala Lys His Asn Gly Arg Gly Ile Asp Gly
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Ile Ala Pro Gly Ala Gln Leu Tyr Ala Val Lys Ala Leu Asp Arg Asn
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 Gly Ala Gly Asp Leu Lys Gly Ile Leu Gln Gly Ile Asp Trp Ser Ile
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 Gln His Gly Ile Asp Ile Ile Asn Met Ser Leu Val Val Ser Gly Asp
 225 230 235 240
 Ser Gln Val Leu His Asp Ala Val Asp Lys Ala Tyr Lys Arg Gly Ile
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 Tyr Pro Ala Ala Tyr Ser Ser Val Ile Ala Val Ser Ala Thr Asn Glu
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 Ala Asp Ala Asp Lys Pro Ala Leu Lys Lys Arg Leu Asn Thr Val Lys
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 Gln Lys Lys Lys Thr Asn Ala Asp Ser Ala Gln Lys Ala Val Asn Glu
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Leu Asp Ser Gly Thr Phe Lys Thr Asn Leu Gln Lys Arg Ile Asn Ala
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Glu Lys Ala Ala Thr Asp Ser Asn Leu Gly Lys Ala Gln Lys Ala Ile
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Asn Glu Leu Pro Ala Gly Lys Asp Lys Ser Asn Leu Gln Lys Arg Leu
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Ala Ala Lys Ala Lys Val Lys Thr Ala Glu Gln Lys Arg Thr Lys Lys
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His Leu Val Ser Thr Gly Lys Leu Asp Leu Asn Lys Asn Ile Ser Gln
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Tyr Leu Pro Asp Phe Lys Asp His Pro Glu Asp Asp Val Lys Gly Lys
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Ala Ser Trp Asn Tyr Tyr Asp Pro Lys Ser Ala Gly His Leu Tyr Ser
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Gln Ser Arg Ser Lys Thr Leu Glu Tyr Leu Val Lys Thr Pro Leu Ala
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Leu Gly Leu Ile Ile Glu Lys Ile Thr Asn Glu Arg Leu Asp Thr Phe
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Val Glu Asn Arg Phe Tyr Arg Pro Leu Gly Leu Arg His Thr Leu Phe
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 Thr Tyr Thr Leu Gln Gly Glu Val His Asp Glu Lys Ala Phe Tyr Ser
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 Met Glu Gly Val Ser Gly His Ala Gly Leu Phe Ser Thr Val Asp Asp
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Gln Glu Gly Glu Lys Thr Ser Ala Val Ala Leu Phe Phe Ser Gln Phe
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gct	ctg	ccg	ctg	ccg	ctt	gtc	ccg	ata	cag	att	ctg	tgg	gtc	aac	ctt	2572	
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10294.000.ST25.txt

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 Asp Asp Val Met Gln Arg Lys Pro Arg Ser Pro Lys Glu Gly Val Phe
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 gca agg ggg ctc ggc tgg aag gtc gta tcg cgc gga ttc tta atc gga 2716
 Ala Arg Gly Leu Gly Trp Lys Val Val Ser Arg Gly Phe Leu Ile Gly
 765 770 775
 atc gcg aca ctc ggg gcg ttt atg ttc att tat aac cgc aat cca gaa 2764
 Ile Ala Thr Leu Gly Ala Phe Met Phe Ile Tyr Asn Arg Asn Pro Glu
 780 785 790
 gcg ctt gag tat gca cag acg gtt gca ttt gca acg ctc gtc ctt gcg 2812
 Ala Leu Glu Tyr Ala Gln Thr Val Ala Phe Ala Thr Leu Val Leu Ala
 795 800 805
 cag ctg atc cac gtg ttc gac tgc cga agc gag cgg tcc atc ttt gac 2860
 Gln Leu Ile His Val Phe Asp Cys Arg Ser Glu Arg Ser Ile Phe Asp
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 825 830 835 840
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 Ile Leu Leu Met Leu Val Val Ile Tyr Tyr Pro Pro Leu Gln Pro Ile
 845 850 855
 ttt cat acg gtt ccg att tta atg gca gac tgg ctc ctg att gtc gga 3004
 Phe His Thr Val Pro Ile Leu Met Ala Asp Trp Leu Leu Ile Val Gly
 860 865 870
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 Lys Asn
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<211> 890

<212> PRT

<213> Bacillus licheniformis

<400> 26

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Val Ala Leu Phe Phe Ser Gln Phe Lys Asp Phe Met Val Leu Val Leu
 50 55 60
 Leu Ala Ala Thr Leu Ile Ser Gly Phe Leu Gly Glu Tyr Ile Asp Ala
 65 70 75 80
 Ile Ala Ile Ile Ala Ile Ile Phe Val Asn Gly Ile Leu Gly Phe Phe
 85 90 95
 Gln Glu Arg Arg Ala Glu Arg Ser Leu Glu Ala Leu Lys Glu Leu Ser
 100 105 110
 Ala Pro Gln Val Ala Val Leu Arg Glu Gly Asn Trp Val Lys Ile Pro
 115 120 125
 Ser Lys Glu Leu Val Pro Gly Asp Val Val Arg Phe Ala Ser Gly Asp
 130 135 140
 Arg Ile Gly Ala Asp Leu Arg Leu Val Glu Thr Lys Ser Leu Glu Ile
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 Glu Glu Ser Ala Leu Thr Gly Glu Ser Leu Pro Val Ser Lys Gln Ala
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 Asp Ala Phe Gln Ala Ser Asp Val Ser Leu Gly Asp Leu Lys Asn Met
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 Ala Phe Met Gly Thr Leu Val Thr Arg Gly Ser Gly Ile Gly Val Val
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 Ile Gly Thr Gly Met Asn Ser Ala Met Gly Lys Ile Ala Asp Met Leu
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 225 230 235 240
 Leu Gly Lys Ile Leu Ile Val Ala Ala Leu Phe Leu Thr Leu Leu Val
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 Val Ala Ala Gly Val Ile Gln Gly His Asp Leu Tyr Ser Met Phe Leu
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 Ala Gly Val Ser Leu Ala Val Ala Ala Ile Pro Glu Gly Leu Pro Ala
 275 280 285
 Ile Val Thr Val Ala Leu Ser Leu Gly Val Gln Arg Met Ile Arg Gln
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 Lys Ser Ile Val Arg Lys Leu Pro Ala Val Glu Thr Leu Gly Cys Ala
 305 310 315 320

Ser Ile Ile Cys Ser Asp Lys Thr Gly Thr Met Thr Gln Asn Lys Met
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 Thr Val Thr His Val Trp Ser Gly Gly Lys Ile Trp Asn Val Ser Gly
 340 345 350
 Ile Gly Tyr Glu Pro Glu Gly Ser Phe Ser Met Asn Gly Arg Asp Val
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 Gln Ala Lys His His Lys Pro Leu Gln Gln Val Leu Leu Phe Gly Ala
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 Leu Cys Asn Ser Ser Ser Ile Ile Glu Lys Asp Gly Glu Phe Arg Leu
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 Asp Gly Asp Pro Thr Glu Gly Ala Leu Leu Thr Ala Ala Arg Lys Ala
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 Gly Phe Thr Asp Lys Tyr Val Asp Glu His Phe Lys Ile Ile Glu Glu
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 Lys Ser Gly Lys Arg Phe Val Ile Thr Lys Gly Ala Pro Asp Val Leu
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 Met Lys Arg Ser Ser His Thr Leu Thr Glu Glu Lys Arg Glu Ile Phe
 465 470 475 480
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 485 490 495
 Ser Gln Ala Leu Arg Thr Ile Ala Val Ala Tyr Lys Pro Ile Lys Asp
 500 505 510
 Thr Glu Asn Pro Pro Leu Glu Lys Ala Glu Ser Gly Leu Thr Phe Ile
 515 520 525
 Gly Leu Leu Gly Met Ile Asp Pro Pro Arg Pro Glu Val Lys Thr Ala
 530 535 540
 Ile Lys Glu Cys Arg Glu Ala Gly Ile Lys Thr Val Met Ile Thr Gly
 545 550 555 560
 Asp His Val Ile Thr Ala Thr Ala Ile Ala Lys Asp Leu Gly Leu Leu
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 Pro Pro Arg Gly Lys Val Met Asp Gly Gln Met Leu Asn Glu Leu Ser
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Gln Glu Glu Leu Ala Glu Ile Val Asp Asp Val Tyr Val Phe Ala Arg
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Val Ser Pro Glu His Lys Leu Lys Ile Val Thr Ala Tyr Gln Glu Asn
610 615 620

Gly His Ile Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Pro Ala
625 630 635 640

Ile Lys Gln Ala Asp Ile Gly Ile Ser Met Gly Ile Thr Gly Thr Asp
645 650 655

Val Ala Lys Glu Ala Ser Ser Leu Ile Leu Val Asp Asp Asn Phe Ala
660 665 670

Thr Ile Lys Ser Ala Ile Lys Glu Gly Arg Asn Ile Tyr Glu Asn Ile
675 680 685

Arg Lys Phe Ile Arg Tyr Leu Leu Ala Ser Asn Val Gly Glu Ile Leu
690 695 700

Val Met Leu Phe Ala Met Leu Leu Ala Leu Pro Leu Pro Leu Val Pro
705 710 715 720

Ile Gln Ile Leu Trp Val Asn Leu Val Thr Asp Gly Leu Pro Ala Met
725 730 735

Ala Leu Gly Met Asp Gln Pro Glu Asp Asp Val Met Gln Arg Lys Pro
740 745 750

Arg Ser Pro Lys Glu Gly Val Phe Ala Arg Gly Leu Gly Trp Lys Val
755 760 765

Val Ser Arg Gly Phe Leu Ile Gly Ile Ala Thr Leu Gly Ala Phe Met
770 775 780

Phe Ile Tyr Asn Arg Asn Pro Glu Ala Leu Glu Tyr Ala Gln Thr Val
785 790 795 800

Ala Phe Ala Thr Leu Val Leu Ala Gln Leu Ile His Val Phe Asp Cys
805 810 815

Arg Ser Glu Arg Ser Ile Phe Asp Arg Asn Pro Phe Glu Asn Ile Tyr
820 825 830

Leu Leu Gly Ala Val Leu Ser Ser Ile Leu Leu Met Leu Val Val Ile
835 840 845

Tyr Tyr Pro Pro Leu Gln Pro Ile Phe His Thr Val Pro Ile Leu Met
850 855 860

Ala Asp Trp Leu Leu Ile Val Gly Met Ser Ala Ile Pro Thr Phe Leu
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<212> DNA

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<220>

<221> CDS

<222> (501)..(3122)

<223>

<400> 27

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taaaagaaat ttaccgtggt ttacagggtg acggcacgct gtttctcgct gtgcatctgg	180
aaggggcaaat gaaaaaatcg aaaaaaacia aaggcttttc cttatactca gaagagcaaa	240
tcaagcaact gcttgaggaa agccatttca gagacatcac ggtacatatg aacaaaaatt	300
actgctgcat ttctgcggta aaatcatgaa ctttgtatga tcatcccttt caatacggaa	360
gggatttttt atgttttgata gagttgaaac tggatcttaa atatcatatt tttgattttt	420
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tatatatttcc ggagggtattt atg aac aaa agg atc gtg aaa agt tca att gtt	533
Met Asn Lys Arg Ile Val Lys Ser Ser Ile Val	
1 5 10	
ttc ttt ctc ctt gcc gca tta att ttt ggc cag ctg cct tta ccg aag	581
Phe Phe Leu Leu Ala Ala Leu Ile Phe Gly Gln Leu Pro Leu Pro Lys	
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Thr Met Ala Ala Glu Asp Ser Val Pro Asn Asn Glu Thr Thr Leu Thr	
30 35 40	
agc gcg tcc cct gtt gaa gct tcg ttt caa agc gat gac gag gtg cat	677
Ser Ala Ser Pro Val Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His	
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tgg tat aaa gtc aat cct tca aat cag gaa atc gca aac tat acg cac	725
Trp Tyr Lys Val Asn Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His	
60 65 70 75	
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ggc Gly	tac Tyr	tcc Ser 110	tat Tyr	gaa Glu	aat Asn	aat Asn	cct Pro 115	gct Ala	tta Leu	atc Ile	gat Asp	ttt Phe 120	ccg Pro	att Ile	gcc Ala	869
tgg Trp	aaa Lys 125	ggt Gly	cct Pro	tac Tyr	tac Tyr	ata Ile 130	aaa Lys	gta Val	gaa Glu	aat Asn	cac His 135	cat His	gat Asp	gag Glu	gaa Glu	917
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ccc Pro	ctc Leu	ggt Gly 350	aaa Lys	agc Ser	aaa Lys	acg Thr	gca Ala 355	ttt Phe	aaa Lys	gat Asp	atg Met	tac Tyr 360	gtt Val	gtg Val	gaa Glu	1589

10294.000.ST25.txt

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ctt Leu	gtc Val 605	tcg Ser	gac Asp	tac Tyr	tcc Ser	aat Asn 610	tat Tyr	gga Gly	aaa Lys	ggt Gly	ctc Leu 615	gat Asp	atg Met	gtg Val	gca Ala	2357
ccg Pro 620	gga Gly	acc Thr	gat Asp	att Ile	cca Pro 625	agc Ser	ctc Leu	gtt Val	ccg Pro	gac Asp 630	ggg Gly	aat Asn	gtc Val	act Thr	tat Tyr 635	2405

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cca aac ccg gat tat gac ctg gat ata gaa ccg gct gca caa att ccc Pro Asn Pro Asp Tyr Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro 685 690 695	2597
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gcc agc gtt ttt gag ctg aac atg aag gtt cat ccc gtt tta aac cgc Ala Ser Val Phe Glu Leu Asn Met Lys Val His Pro Val Leu Asn Arg 720 725 730	2693
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gtc gcg gca tcg ggc cat cag gcg gaa acc tcg ctc aga acc gtc gtg Val Ala Ala Ser Gly His Gln Ala Glu Thr Ser Leu Arg Thr Val Val 780 785 790 795	2885
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<211> 874

<212> PRT

<213> Bacillus licheniformis

<400> 28

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Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His Trp Tyr Lys Val Asn
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Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His Phe Arg Val Lys Leu
 65 70 75 80

Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr Ser Ser Leu Glu Asn
 85 90 95

Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn Gly Tyr Ser Tyr Glu
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Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala Trp Lys Gly Pro Tyr
 115 120 125

Tyr Ile Lys Val Glu Asn His His Asp Glu Glu Asn Glu Thr Thr Ser
 130 135 140

Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu Gly Val Thr Leu Pro
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Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro Ala Glu Leu Ser Val
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 385 390 395 400
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 Gln Leu Gln Lys Leu Met Lys Gly Lys Lys Leu Lys Asp Thr Val Ile
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Ala Val Val Asp Thr Gly Val Asp His Thr Leu Ala Asp Leu Ser Gly
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 Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val Gly Arg Thr Ala Asp
 465 470 475 480
 Ala Met Asp Asp Asn Gly His Gly Thr His Val Ser Gly Ile Ile Ala
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 Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser Arg Val Met Glu Tyr
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 Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp Leu Val Ser Asp Tyr
 595 600 605
 Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala Pro Gly Thr Asp Ile
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 Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr Met Ser Gly Thr Ser
 625 630 635 640
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 645 650 655
 Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser Leu Leu Thr Glu Thr
 660 665 670
 Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn Pro Asn Pro Asp Tyr
 675 680 685
 Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro Gly Tyr Asp Phe Val
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 Ser Gly Trp Gly Arg Leu Asn Val Phe His Ala Ala Ser Val Phe Glu
 705 710 715 720

Leu Asn Met Lys Val His Pro Val Leu Asn Arg His Thr Ala Val Thr
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Gly Thr Ala Lys Ser Gly Val Thr Val Lys Ile Leu Arg Gly Lys Gln
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Val Leu Gly Thr Gly Thr Ala Gly Lys Ser Gly Ala Phe Ser Val Lys
 755 760 765

Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His Val Ala Ala Ser Gly
 770 775 780

His Gln Ala Glu Thr Ser Leu Arg Thr Val Val Glu Lys Ala Pro Lys
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Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp Thr Ala Val Thr Gly
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Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys Asn Ala Tyr Lys Lys
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Val Ile Ala Gln Gly Ile Ala Asp Ala Ser Val Ser Val Lys Val Lys
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 Val Ser Ser Leu Val Pro Leu Met Ile Met Val Cys Phe Leu
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 Ile Leu Leu Leu Ala Leu Asp Phe His Phe Gly Arg Lys Ala Phe Glu
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 Lys Lys Ala Tyr Glu Pro Val Phe Ser Glu Lys Lys Ser Asp Ile Glu
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 ctg att cat aat gga gaa gac ttg tgt gag cgg ctg ctg gat gac atc 675
 Leu Ile His Asn Gly Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile
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 Arg Gln Ala Glu Ser Ser Val His Val Met Phe Tyr Ile Val Lys Asn
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 Asp Asp Ile Ser Leu Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys
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att Ile	gaa Glu	cac His	gcc Ala	gag Glu	ctt Leu	ctg Leu	aca Thr	aag Lys	gag Glu	cgg Arg	tat Tyr	gcg Ala	aag Lys	cgg Arg	ccg Pro	1635
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<400> 30

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 Ala Glu Ser Ser Val His Val Met Phe Tyr Ile Val Lys Asn Asp Asp
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 Lys Lys Thr Leu Ser Gly Leu Lys Gln Ser Gly Val His Val Phe Phe
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 Ala Asn Lys Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn Ala Arg
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 Gly Phe Asn Ile Ala Lys Glu Tyr Leu Gly Lys Lys Ala Glu Phe Gly
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 Pro Trp Lys Asp Tyr His Leu Arg Met Thr Gly Glu Gly Val Ala Asp
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 Leu Gln His Ile Phe Ile Ser Asp Phe Lys Arg Glu Ala Pro Gln Ala
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 Lys Pro Ala Asn Ser Val Phe Pro Pro Leu Gln Gln Gly Ala Val Thr
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 His Thr Thr His Ala Thr Lys Gly Phe Ser Leu Glu Glu Lys Tyr Ile
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 Ser Phe Ile Glu Gln Ala Lys Glu Arg Ile Met Ile Cys Thr Pro Tyr
 245 250 255

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Tyr Ile Pro Ser₂₆₀ Pro Ala Leu Gln₂₆₅ Gln Ala Val Leu Ser Ala₂₇₀ Arg Glu
 Arg Gly Val₂₇₅ Ile Val Ser Val Leu₂₈₀ Val Pro Met Lys₂₈₅ Pro Asp His Pro
 Leu Val₂₉₀ Lys Glu Ala Ala Tyr₂₉₅ Thr His Phe Pro Ala₃₀₀ Leu Leu Lys Ala
 Gly₃₀₅ Cys Tyr Ile Tyr Arg₃₁₀ Tyr Tyr Arg Gly₃₁₅ Tyr His Ala Lys₃₂₀ Ala
 Leu Ile Val Asp₃₂₅ Asp Arg His Val Met Ile₃₃₀ Gly Thr Ser Asn Phe₃₃₅ Asp
 Asn Arg Ser Leu₃₄₀ Phe Leu Asn Asp Glu₃₄₅ Val Asn Val Val Ile₃₅₀ His Asp
 Lys Asp Trp₃₅₅ Thr Lys Gln Phe Phe₃₆₀ Asp Val Val Lys Glu₃₆₅ Ser Ile Glu
 His Ala Glu Leu Leu Thr Lys₃₇₅ Glu Arg Tyr Ala Lys₃₈₀ Arg Pro Val Met
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Cys	Leu	Phe	Phe	Gln	Leu	Tyr	Trp	Lys	Arg	Asn	Arg	Tyr	Val	Leu	Leu		
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ggg Gly	ctg Leu	gtc Val	tat Tyr	cat His	aaa Lys	cgg Arg	acg Thr	aag Lys	ctt Leu	gta Val	atc Ile	ggt Val	tca Ser	gac Asp	ggg Gly	1944
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tttggcaaac	gccataatgc	aggaagagct	gaaacatcac	attgaccggc	tgaaagaaga											2688
ttaccagact	gtcctcattt	taagagagtt	tcaagagctg	tcatacgagg	aaatagcgga											2748
agtgctgaat	tggaactgt	caaaggtaaa	aaccaatctt	caccggggccc	gcctggagct											2808
gaaaaaaagc	ttggaaggca	gggaggttta	acaatatgaa	atgccatctt	gtaagagatt											2868
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<210> 32

<211> 645

<212> PRT

<213> Bacillus licheniformis

<400> 32

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Glu Arg Tyr Phe Val Leu Ser Arg Gln Ser Met Leu Val Ile Gln Trp
 20 25 30
 Cys Val Thr Gly Leu Val Leu Leu Tyr Ala Val Ser Phe His Pro Lys
 35 40 45
 Val Cys Arg Arg Arg Leu Phe Phe Tyr Ala Gly Ile Val Leu Arg Leu
 50 55 60
 Ile Leu Val Gly Ala Leu Ser Phe Glu Leu Ala His Gln Met Lys Ala
 65 70 75 80
 Ala Glu Phe Ser Asn Leu Tyr Ile Asp Glu Gln Asp Ala Leu Leu Pro
 85 90 95
 Phe Met Gln Phe Leu Leu Phe Gly Tyr Ile Leu Leu Val Ser Phe His
 100 105 110
 Tyr Met Met Thr Leu Ala Glu Lys Gly Gly Lys Gly Leu Phe Phe Ala
 115 120 125
 Phe Asp Ile Ala Val Met Ala Met Pro Leu Phe Gln Ser Leu Phe Ser
 130 135 140
 Phe Ala Ala Tyr Leu Lys Glu Phe Gly Ala Glu Glu Leu Glu Glu Leu
 145 150 155 160
 Pro Leu Val Leu Leu Leu Ile Val Gly Ile Pro Gly Leu Met Ile Cys
 165 170 175
 Leu Phe Phe Gln Leu Tyr Trp Lys Arg Asn Arg Tyr Val Leu Leu Leu
 180 185 190
 Ile Phe Tyr Ile Val Thr Ile Gly Gly Phe Phe Ile Lys Lys Leu Gly
 195 200 205
 Tyr Glu Phe Phe Pro Leu Asn Val Phe Leu Thr Met Ile Gly Phe Leu
 210 215 220
 Met Thr Tyr His Leu Leu Asn Asp Ser Arg Lys Pro Leu Leu Met Val
 225 230 235 240
 Lys Arg Val Leu Ala Ala Gly Thr Ala Val Phe Phe Thr Leu His Leu
 245 250 255
 Asn Pro Phe Tyr Asn Leu Ala Asp Ala Ala Phe Thr Ile Ser His Pro
 260 265 270
 Glu Val Ser Asp Val Val Asp Ala Asn Phe Arg Pro Val Ser Val Lys
 275 280 285

Glu Ala Lys Gln Thr Val Ser Ser Phe Phe Pro Thr Glu Ser Phe Ile
 290 295 300
 Tyr Leu Ser Ala Thr Asn Gln Asp Phe His Asn Val Tyr His Phe Lys
 305 310 315 320
 Thr Lys Asp Tyr Asp Ala Asp Val Asp Gly Trp Thr Gly Met Ile Thr
 325 330 335
 Asn Tyr His Asn Gln Lys Lys Pro Ser Gly Asn Ile Leu Ser Gly Gln
 340 345 350
 Ala Tyr Ile Lys Arg Ser Lys Gln Phe Leu Arg Glu His Gly Arg Glu
 355 360 365
 Leu Asp Lys Gln Ile Lys Ala Lys Val Ser Arg Asp Asp Gly Glu Ala
 370 375 380
 Thr Val Glu Phe Tyr Arg Glu Gly Glu Asp Pro Glu Leu Ser Thr Met
 385 390 395 400
 Trp Phe Thr Trp Arg Lys Glu Thr Leu Met Gly Phe His Glu Asp Ala
 405 410 415
 Ser Val Tyr Ser Leu Glu Ser Val Asn Gln Ala Arg Val Ser Gly Glu
 420 425 430
 Asp Ile Glu Arg Gly Val Glu Ala Val Tyr Arg Lys Leu Gly Ile Pro
 435 440 445
 Val Ser Ser Tyr Arg Leu Thr Asp Ile Asp Leu Leu Phe Pro Phe Ser
 450 455 460
 Leu Asn Ser Ala Ser Ile Asn Ile Lys Thr Ser Asp Gly Met Gly Met
 465 470 475 480
 Glu Phe His Pro Val Thr Gly Ala Leu Thr Ala Ile Ser Ile Lys Ser
 485 490 495
 Glu Ser Ala Leu Pro Tyr Arg Gly Gln Glu Leu Glu Lys Arg Leu Leu
 500 505 510
 Ser Leu Phe Asp Gln Asp Ile Ser Asn Leu Lys Arg Val Glu Leu Glu
 515 520 525
 Lys Asp Leu Ile Glu Phe Gln Lys Lys Glu Ser Asp Ala Val Leu Asn
 530 535 540
 Thr Val Trp Thr Met Thr Lys His Glu Glu Gly Ala Tyr Leu Thr Val
 545 550 555 560

10294.000.ST25.txt

Arg Lys Asn Phe Gln Lys Ala Asp Glu Lys Pro Pro Tyr Thr Tyr Ala
565 570 575

Asp Gly Glu Lys Ala Phe Gln Lys Val Ser Glu Arg Tyr Gln Lys Gly
580 585 590

Leu Val Tyr His Lys Arg Thr Lys Leu Val Ile Val Ser Asp Gly Asp
595 600 605

Gln Lys Ser Arg Tyr Ala Trp Leu Val Ile Ile Gln Pro Phe Gly Ser
610 615 620

Asn Glu His Asp Ala Tyr Leu Val Asp Ala Glu Thr Asp Glu Val Lys
625 630 635 640

His Phe Asp Asp Lys
645

<210> 33

<211> 1712

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1211)

<223>

<400> 33
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aattctgcag aggaatgctt tgctcctctt ttctactttt tttctaagca tacggatatc 120
ttatatgacg gctgcatcga ctttgccatt gaggcataatt tgctgggagc cgagtacggg 180
aagttcggct atcacggaga acccgttcat cgagcgaatga tccgctcaga aaaagaagaa 240
aaacagctac tgcacgagct ttatgaatat gctgtcagct ggtctgaggc ttttaatggt 300
caagctgctt atgaaccgct ctattatgcc tgcgaatact tcatccaaag ctggtggaag 360
gaaggcttca gccagcggga aagacgcttt aagcttcggc tcagataaaa caaagtttta 420
tgaaaaagtg aggccaagct taatcatatt tcctttcctt gtcccatatc ttgtagtaag 480
gacgagcggg agggaaaggg atg aag aaa aaa ata aaa tgg ctc ggg ttt tta 533
Met Lys Lys Lys Ile Lys Trp Leu Gly Phe Leu
1 5 10
ctc ggc ttt gtc gtt tta tta tgt tta ttt caa tat caa ttc aac aat 581
Leu Gly Phe Val Val Leu Leu Cys Leu Phe Gln Tyr Gln Phe Asn Asn
15 20 25

10294.000.ST25.txt

gat gat tct tgg cgg tca tgg aat ctt ccg ctg agc ggc aaa atc att Asp Asp Ser Trp Arg Ser Trp Asn Leu Pro Leu Ser Gly Lys Ile Ile 30 35 40	629
tat att gat cct gga cac ggg ggc gcc gat gga ggg gca tca agc ggt Tyr Ile Asp Pro Gly His Gly Gly Ala Asp Gly Gly Ala Ser Ser Gly 45 50 55	677
gaa ctc ctt gaa aaa gac gtg gct ctt gaa gta tcc cta aga atc agg Glu Leu Leu Glu Lys Asp Val Ala Leu Glu Val Ser Leu Arg Ile Arg 60 65 70 75	725
gac tat ctc cag gag cag ggc gcc ttg gtg atg ctg acg cgg gag gac Asp Tyr Leu Gln Glu Gln Gly Ala Leu Val Met Leu Thr Arg Glu Asp 80 85 90	773
gat cat gat ctc gct cct gaa gaa acg agg gga ctc agc aga aga aaa Asp His Asp Leu Ala Pro Glu Glu Thr Arg Gly Leu Ser Arg Arg Lys 95 100 105	821
gct gaa gac ttg cgg aag agg gtc gat atg atc aac aat tct gaa gcc Ala Glu Asp Leu Arg Lys Arg Val Asp Met Ile Asn Asn Ser Glu Ala 110 115 120	869
gat ctt tac ctc agc atc cat ttg aat gcg att cct tcc gcg cga tgg Asp Leu Tyr Leu Ser Ile His Leu Asn Ala Ile Pro Ser Ala Arg Trp 125 130 135	917
agc ggt gcg caa agc ttc tat tac ggg caa tat gaa gag aat gaa cgg Ser Gly Ala Gln Ser Phe Tyr Tyr Gly Gln Tyr Glu Glu Asn Glu Arg 140 145 150 155	965
gcc gcc aag ttt att cag gat gaa tta aga cat aat ctt gaa aac acg Ala Ala Lys Phe Ile Gln Asp Glu Leu Arg His Asn Leu Glu Asn Thr 160 165 170	1013
acg cgg aag gca aag cgg ata cac gga att tat ttg atg caa aat gtt Thr Arg Lys Ala Lys Arg Ile His Gly Ile Tyr Leu Met Gln Asn Val 175 180 185	1061
aaa aag ccc ggg gcc ctt gtc gaa atc ggg ttt ttg tct aac ccg gaa Lys Lys Pro Gly Ala Leu Val Glu Ile Gly Phe Leu Ser Asn Pro Glu 190 195 200	1109
gag gca aaa cag ctg gcc aag ccc aaa tat cag gac aaa atc gca gca Glu Ala Lys Gln Leu Ala Lys Pro Lys Tyr Gln Asp Lys Ile Ala Ala 205 210 215	1157
tcc gtt tat aaa ggc gta ttg cgc tac ttt aca gaa gac aga gac cct Ser Val Tyr Lys Gly Val Leu Arg Tyr Phe Thr Glu Asp Arg Asp Pro 220 225 230 235	1205
cct gaa taagagggtt tctttttgtg tcaaagacac tataaggaaa gatatgctat Pro Glu	1261
acttatttttg taaacgaata caacaaaggg tgagatcaat gttgcgagaa gacgatgtaa	1321
aaaagatagt cggcgatttg gacgagccat ttcttcacaa gccgctcaga gagctggatg	1381
ccgtaaaaga aattaaata aaacccgaaa aacggcacgt cagcgtaaag gtggcgctcg	1441
caaaaacggg atctgccgaa caaatgcagc ttcagcagga aatcgtcata cggttgaaag	1501
aagccggtgc agagacgggc ggcctgcgtt ttgaggagct gccgaagaa gtcgtaatga	1561
gttatcaaga gtctgccaaa gggcaggatc aatctctgct gaatagtga aaacagcctg	1621

10294.000.ST25.txt

tgttttttagc tgtggcaagc ggcaaaggcg gcgtcggcaa gtcgacgggtg tcggtcaatt 1681
 tggctgtgtc cctggcgcgga atcggaaaga a 1712

<210> 34

<211> 237

<212> PRT

<213> Bacillus licheniformis

<400> 34

Met Lys Lys Lys Ile Lys Trp Leu Gly Phe Leu Leu Gly Phe Val Val
 1 5 10 15
 Leu Leu Cys Leu Phe Gln Tyr Gln Phe Asn Asn Asp Asp Ser Trp Arg
 20 25 30
 Ser Trp Asn Leu Pro Leu Ser Gly Lys Ile Ile Tyr Ile Asp Pro Gly
 35 40 45
 His Gly Gly Ala Asp Gly Gly Ala Ser Ser Gly Glu Leu Leu Glu Lys
 50 55 60
 Asp Val Ala Leu Glu Val Ser Leu Arg Ile Arg Asp Tyr Leu Gln Glu
 65 70 75 80
 Gln Gly Ala Leu Val Met Leu Thr Arg Glu Asp Asp His Asp Leu Ala
 85 90 95
 Pro Glu Glu Thr Arg Gly Leu Ser Arg Arg Lys Ala Glu Asp Leu Arg
 100 105 110
 Lys Arg Val Asp Met Ile Asn Asn Ser Glu Ala Asp Leu Tyr Leu Ser
 115 120 125
 Ile His Leu Asn Ala Ile Pro Ser Ala Arg Trp Ser Gly Ala Gln Ser
 130 135 140
 Phe Tyr Tyr Gly Gln Tyr Glu Glu Asn Glu Arg Ala Ala Lys Phe Ile
 145 150 155 160
 Gln Asp Glu Leu Arg His Asn Leu Glu Asn Thr Thr Arg Lys Ala Lys
 165 170 175
 Arg Ile His Gly Ile Tyr Leu Met Gln Asn Val Lys Lys Pro Gly Ala
 180 185 190
 Leu Val Glu Ile Gly Phe Leu Ser Asn Pro Glu Glu Ala Lys Gln Leu
 195 200 205

Val Leu Arg Tyr Phe Thr Glu Asp Arg Asp Pro Pro Glu
225 230 235

<213> Bacillus licheniformis

<223>

<400>	35												
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aagaatctag	ttgagcgg	gtg	gagcaggg	ga	ttccttatta	tgact	gcat	tttgc	acatt		180		
tctccatttt	cctgcaaggt	caaa	agacat	agt	tcttaag	ttttg	gattt	ttggt	gtgtt		240		
tattttttgt	ttcacaaact	tta	aggtaat	ttta	agaaag	aggcg	atcct	gccaa	cccta		300		
aacaggggtt	ttcgaacaga	atg	tcaaata	gatt	agatat	ttcata	agaa	caagg	ggggaa		360		
ttgtctgttt	gtgatgaata	aagg	aggacg	ggc	ggaattt	ctgtc	aggat	gctc	agctgg		420		
gttcttagaa	aaaaatgcgg	ctaa	atatat	attt	atagat	tgtaa	acgct	gtctt	gtcct		480		
cgaccaacag	ggggatgaag	atg	aag	aag	ctg	tta	gtt	gtt	tat	gcc	gtg	atg	533
		Met	Lys	Lys	Leu	Leu	Val	Val	Tyr	Ala	Val	Met	
		1				5					10		

ctc tgt ttg ttt ttt ctg tat gtc tac gac tac tcc cgg ggc gat aaa 581
Leu Cys Leu Phe Phe Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys
15 20 25

gcc ggt tct gca gaa gaa agc agg agg cct gcg gcc gca ggc agt ctg 629
Ala Gly Ser Ala Glu Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu
30 35 40

tcc gaa aaa tac gtg atg gtc acg ttt caa tcg gga atc gaa tat tgg 677
Ser Glu Lys Tyr Val Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp
45 50 55

aag agc ggt ctg aaa ggc ttt gag gat gcc gcg cag ctt ttc aac gtc 725
Lys Ser Gly Leu Lys Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val
60 65 70 75

tct gtc gag tat cgg ggg gcg gcc cat tat gat gtc cat gag caa acg 773

10294.000.ST25.txt

ser val glu tyr arg gly ala ala his tyr asp val his glu gln thr
 80 85 90
 acc gtc ctc gag cag gtg att gca aaa aaa ccg gcg gga atc gct gtt 821
 thr val leu glu gln val ile ala lys lys pro ala gly ile ala val
 95 100 105
 tcg gca ata aac cca aaa gct tta aac cct gtc atc gac aag gcg cac 869
 ser ala ile asn pro lys ala leu asn pro val ile asp lys ala his
 110 115 120
 gag cag ggt att ccg atc gtt tta ttt gat tca gac gcc ccg ctc agc 917
 glu gln gly ile pro ile val leu phe asp ser asp ala pro leu ser
 125 130 135
 aaa gct tct aca tat atc ggc aca aat aat atg gaa gcg ggt gct gtg 965
 lys ala ser thr tyr ile gly thr asn asn met glu ala gly ala val
 140 145 150 155
 gcc gca agg cga atg gcc gaa ttt ttg aat gga aag gga gaa acc gcg 1013
 ala ala arg arg met ala glu phe leu asn gly lys gly glu thr ala
 160 165 170
 gtc att acc cag ccg cag cag tac aat cat cag gaa agg acg aag ggc 1061
 val ile thr gln pro gln gln tyr asn his gln glu arg thr lys gly
 175 180 185
 ttt gaa caa acg atc aag caa aaa tac ccg aac atg aag gtt gcc gcg 1109
 phe glu gln thr ile lys gln lys tyr pro asn met lys val ala ala
 190 195 200
 gtt ttg gac gga aaa ggg gat gag ctg acg tcg aaa aaa gaa gcg gcg 1157
 val leu asp gly lys gly asp glu leu thr ser lys lys glu ala ala
 205 210 215
 aag att ttg gag gaa aat ccg tcc atc aaa gga att ttc acg act gaa 1205
 lys ile leu glu glu asn pro ser ile lys gly ile phe thr thr glu
 220 225 230 235
 gcc aat gga gcg agc ggc gtg gcc cgt gct gtg aag gag gcg gga ctt 1253
 ala asn gly ala ser gly val ala arg ala val lys glu ala gly leu
 240 245 250
 gaa ggg gaa gta tgt atc atc ggc ttt gat aaa gac aag aaa acg ctg 1301
 glu gly glu val cys ile ile gly phe asp lys asp lys thr leu
 255 260 265
 gac ggc atc aaa aac gga tcg att tcc gcg aca atg agc cag gac aca 1349
 asp gly ile lys asn gly ser ile ser ala thr met ser gln asp thr
 270 275 280
 tgg caa atg ggc tat tgg tcg ctg cac atg ctg ttt ttc tca aat cac 1397
 trp gln met gly tyr trp ser leu his met leu phe phe ser asn his
 285 290 295
 cat ctg aag cat gaa cgc ccg ctt ccg gcc gca atc gac aca ggc att 1445
 his leu lys his glu arg pro leu pro ala ala ile asp thr gly ile
 300 305 310 315
 acc atc ata acg aaa gaa aat gtg gca gcc tat tat gcg aat 1487
 thr ile ile thr lys glu asn val ala ala tyr tyr ala asn
 320 325
 gattaaacgt ttgatcaata atgcgccgat ccgtcataag ctgatcagcc ttctcttggt 1547
 aatcagcatg ctgccgacga tcggcctggg cattttatcg ggatgggccg ttgaaaatat 1607
 tattgaaaaa caggtgatcg accaaacact gcagctgacg ggcgaagtga acaagacggc 1667

10294.000.ST25.txt

tgaagtgtat gtcagccaca tgcagaacct gacatatatta atatcaatga atgaagaaat 1727
 ggaagcgttt tttagtcata aaaaggagga tggagaggcg gattataagc gaaggacgtt 1787
 tttgcagggc ctgacttctt tatattccga agcagcgggt attctcgttg tcaatgataa 1847
 ggggtgagatg atcagcaatg agatgtatga acgcacgccg acagatttga caaaagaacc 1907
 atggtatcag gcggctctcg acaatgaagg gattttcaag atgatcgggg agcctgtcaa 1967
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<210> 36

<211> 329

<212> PRT

<213> Bacillus licheniformis

<400> 36

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Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys Ala Gly Ser Ala Glu
 20 25 30

Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu Ser Glu Lys Tyr Val
 35 40 45

Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp Lys Ser Gly Leu Lys
 50 55 60

Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val Ser Val Glu Tyr Arg
 65 70 75 80

Gly Ala Ala His Tyr Asp Val His Glu Gln Thr Thr Val Leu Glu Gln
 85 90 95

Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val Ser Ala Ile Asn Pro
 100 105 110

Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His Glu Gln Gly Ile Pro
 115 120 125

Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser Lys Ala Ser Thr Tyr
 130 135 140

Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val Ala Ala Arg Arg Met
 145 150 155 160

Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala Val Ile Thr Gln Pro
 165 170 175

10294.000.ST25.txt

Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly Phe Glu Gln Thr Ile
180 185 190
Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala Val Leu Asp Gly Lys
195 200 205
Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala Lys Ile Leu Glu Glu
210 215 220
Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu Ala Asn Gly Ala Ser
225 230 235 240
Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu Glu Gly Glu Val Cys
245 250 255
Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu Asp Gly Ile Lys Asn
260 265 270
Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr Trp Gln Met Gly Tyr
275 280 285
Trp Ser Leu His Met Leu Phe Phe Ser Asn His His Leu Lys His Glu
290 295 300
Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile Thr Ile Ile Thr Lys
305 310 315 320
Glu Asn Val Ala Ala Tyr Tyr Ala Asn
325

<210> 37

<211> 2785

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(2282)

<223>

<400> 37

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cggaaaccgc aaacaaagcg aaggcaacgg aattttgtgta tcaagtcaac agcttatctc 120

acagtgattt aaacaagatg ttcggctctc cagatgcacc ggcagaagcg cagaatctga 180

10294.000.ST25.txt

caaaagcggg	tatggcggtt	ttagagaagg	aaaataaata	gatcaaacgg	ccgactcggc	240
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aaatgttaaa	ttcggcctct	tctcacactt	ggcaccctct	tactcataag	acatcgatct	360
gaaaattccc	aaaatataaa	caaaacatta	ataaaatcaa	gccatttgat	taacaaattt	420
acgatacgat	catatagaac	ttgatgattg	ggaaaagcat	tttgagagaa	gattaagagc	480
aaggggagata	tgatgtgaga	atg aaa cga tta agg atg agg aag cat tta ctg				533
		Met Lys Arg Leu Arg Met Arg Lys His Leu Leu				
		1 5 10				
ata gct gtc tgt act ttg gca ctt ctt cta agt tcc ccg att gta agc						581
Ile Ala Val Cys Thr Leu Ala Leu Leu Leu Ser Ser Pro Ile Val Ser						
		15 20 25				
gat gcg agc ccg gca act aaa cca aca act gca gat tcg ccg caa tct						629
Asp Ala Ser Pro Ala Thr Lys Pro Thr Thr Ala Asp Ser Pro Gln Ser						
		30 35 40				
tcc gga ttt ttc gta gac cat tac aaa aat aat atc tct gcc aat acg						677
Ser Gly Phe Phe Val Asp His Tyr Lys Asn Asn Ile Ser Ala Asn Thr						
		45 50 55				
acg gcg gaa tcc aat cct gtc atc ggc ctg ctt tcc gaa ttt aat aaa						725
Thr Ala Glu Ser Asn Pro Val Ile Gly Leu Leu Ser Glu Phe Asn Lys						
		60 65 70 75				
ctt tgg act ccc gga aag aca tgg aat acc ggt act aaa ctg aac agc						773
Leu Trp Thr Pro Gly Lys Thr Trp Asn Thr Gly Thr Lys Leu Asn Ser						
		80 85 90				
agg gtg ctg gat gcc aac att caa aaa gtc gtg gat att gct gaa cgc						821
Arg Val Leu Asp Ala Asn Ile Gln Lys Val Val Asp Ile Ala Glu Arg						
		95 100 105				
cgc acg atg ctt gag gaa aat gct gcc tat ttt gat gat cgg cgg agc						869
Arg Thr Met Leu Glu Glu Asn Ala Ala Tyr Phe Asp Asp Arg Arg Ser						
		110 115 120				
cag agc tac agt ata att gac ggc ctc ggc aag ctt gcc ggc gtc tat						917
Gln Ser Tyr Ser Ile Ile Asp Gly Leu Gly Lys Leu Ala Gly Val Tyr						
		125 130 135				
cga atg aac gcg gga gcg acg aca acg atc acc agc att ccg gca gat						965
Arg Met Asn Ala Gly Ala Thr Thr Thr Ile Thr Ser Ile Pro Ala Asp						
		140 145 150 155				
gcc tcg att aga aaa tac aat gat gaa gga acc aat tcg gcc agc acc						1013
Ala Ser Ile Arg Lys Tyr Asn Asp Glu Gly Thr Asn Ser Gly Ser Thr						
		160 165 170				
agc tct gaa ctt gga aat gtc gta agt ttg gtc aat act tta cgc ggc						1061
Ser Ser Glu Leu Gly Asn Val Val Ser Leu Val Asn Thr Leu Arg Gly						
		175 180 185				
aac tat tct tca tcg aat ccg gct aaa agc tat ttc aac tat ccc cgc						1109
Asn Tyr Ser Ser Ser Asn Pro Ala Lys Ser Tyr Phe Asn Tyr Pro Arg						
		190 195 200				
ccg ttt cgc tgg aaa gac aat tcg atc att gtt cca acg ctt atc ccc						1157
Pro Phe Arg Trp Lys Asp Asn Ser Ile Ile Val Pro Thr Leu Ile Pro						
		205 210 215				
gtc atc aat cct gat ccg aac aaa gac gga ggt ttt cca agc gga cac						1205

10294.000.ST25.txt

Val 220	Ile	Asn	Pro	Asp	Pro 225	Asn	Lys	Asp	Gly 230	Gly	Phe	Pro	Ser	Gly	His 235	
acg Thr	aac Asn	gcc Ala	gca Ala	tat Tyr 240	ctc Leu	agc Ser	gct Ala	ttt Phe	gct Ala 245	atg Met	gcc Ala	tat Tyr	gcg Ala	ata Ile 250	ccg Pro	1253
gag Glu	cgt Arg	tat Tyr	cag Gln 255	gag Glu	ctg Leu	ctg Leu	act Thr	cgc Arg 260	gct Ala	tca Ser	gaa Glu	ctc Leu	ggg Gly 265	cat His	aac Asn	1301
cgg Arg	att Ile	gtt Val 270	gcc Ala	ggg Gly	atg Met	cat His	tcc Ser 275	ccg Pro	ctg Leu	gac Asp	gtc Val	atg Met 280	ggg Gly	gga Gly	cga Arg	1349
gta Val 285	atg Met	gca Ala	aca Thr	gct Ala	ttg Leu	tct Ser 290	gca Ala	gca Ala	atc Ile	ctg Leu	tct Ser 295	gac Asp	ccc Pro	gca Ala	aat Asn	1397
gaa Glu 300	aga Arg	ttg Leu	aag Lys	aaa Lys	acg Thr 305	gct Ala	ttt Phe	gat Asp	gaa Glu	gcc Ala 310	cgc Arg	cgt Arg	aaa Lys	tta Leu	tta Leu 315	1445
acg Thr	caa Gln	acc Thr	ggg Gly	aca Thr 320	gct Ala	gaa Glu	gac Asp	aga Arg	tac Tyr 325	agc Ser	gat Asp	tat Tyr	gag Glu	aag Lys 330	aat Asn	1493
aaa Lys	aaa Lys	caa Gln	tat Tyr 335	acg Thr	gaa Glu	cga Arg	ttg Leu	aca Thr 340	tat Tyr	gga Gly	ttt Phe	cga Arg	caa Gln 345	atg Met	aac Asn	1541
aaa Lys	acc Thr	gcc Ala 350	aaa Lys	cca Pro	atg Met	gca Ala	gtt Val 355	cca Pro	aag Lys	gga Gly	gcc Ala	gaa Glu 360	gtc Val	ctg Leu	ctg Leu	1589
gaa Glu	aca Thr 365	cgt Arg	ttt Phe	cct Pro	tac Tyr	ctt Leu 370	gac Asp	aaa Lys	aag Lys	cag Gln 375	cgc Arg	cgt Arg	tcg Ser	gtt Val	tta Leu	1637
gcc Ala 380	act Thr	acc Thr	ggg Gly	ctt Leu	ccg Pro 385	gcc Ala	ggc Gly	tac Tyr	cct Pro	gtt Val 390	ctt Leu	gat Asp	gat Asp	cga Arg	gaa Glu 395	1685
gga Gly	tgg Trp	gga Gly	agg Arg	ctt Leu 400	aat Asn	ctc Leu	ttt Phe	tcc Ser	gcg Ala 405	gca Ala	gat Asp	ggg Gly	tat Tyr	ggg Gly 410	gct Ala	1733
ttt Phe	acc Thr	aaa Lys	aat Asn 415	gtt Val	acc Thr	gtg Val	acc Thr	atg Met 420	gat Asp	tcc Ser	gca Ala	aaa Lys	ggc Gly 425	ggc Gly	ttc Phe	1781
cat His	aca Thr	gcc Ala 430	gat Asp	cgc Arg	tgg Trp	cgc Arg	aac Asn 435	gac Asp	atc Ile	tcc Ser	ggc Gly	acc Thr 440	gga Gly	aag Lys	ctg Leu	1829
acc Thr	aaa Lys 445	aaa Lys	ggg Gly	aca Thr	ggc Gly	gct Ala 450	ttg Leu	aag Lys	ctg Leu	gaa Glu	ggg Gly 455	gat Asp	aat Asn	aca Thr	tat Tyr	1877
tcc Ser 460	ggc Gly	ggg Gly	aca Thr	cgg Arg	att Ile 465	gat Asp	caa Gln	gga Gly	aca Thr	ctt Leu 470	gag Glu	ggc Gly	ggg Gly	tcg Ser	gag Glu 475	1925
aca Thr	gct Ala	ttc Phe	ggg Gly 480	aga Arg	ggg Gly	gat Asp	gtt Val	gca Ala	cta Leu 485	aac Asn	gga Gly	ggc Gly	atc Ile	ctt Leu 490	aag Lys	1973
gaa	gat	gcg	ccg	gga	aaa	ctg	atc	atc	gaa	gga	gac	tac	aaa	caa	tct	2021

10294.000.ST25.txt

Glu Asp Ala Pro Gly Lys Leu Ile Ile Glu Gly Asp Tyr Lys Gln Ser
495 500 505

gct aaa gga ata ctt gaa ctt cag ctc agc ggc aaa aaa gat cag ttg 2069
Ala Lys Gly Ile Leu Glu Leu Gln Leu Ser Gly Lys Lys Asp Gln Leu
510 515 520

aaa att aag gga aaa gca aga ttg aaa ggg aca ttg cgt ctc aat ttt 2117
Lys Ile Lys Gly Lys Ala Arg Leu Lys Gly Thr Leu Arg Leu Asn Phe
525 530 535

acg gac aat tac gta ccg gct gac gga tcg gcg atc ata acc ttc cgc 2165
Thr Asp Asn Tyr Val Pro Ala Asp Gly Ser Ala Ile Ile Thr Phe Arg
540 545 550 555

aag cgt cat gga tca ttt tct tcc gtc gag acc agt gga ttg cca agc 2213
Lys Arg His Gly Ser Phe Ser Ser Val Glu Thr Ser Gly Leu Pro Ser
560 565 570

aag tat aaa gtg aag atc atc tat aaa tcc aac agt att cag ttg aaa 2261
Lys Tyr Lys Val Lys Ile Ile Tyr Lys Ser Asn Ser Ile Gln Leu Lys
575 580 585

gtt gag caa aag ggg aga agc tgatctgcaa gaggattcac tcaaaagctg 2312
Val Glu Gln Lys Gly Arg Ser
590

caagctggcg catactgccg ccagcttgct tttagttttg atgaaatcac agccagaatg 2372

gctgtacatc ttgaatgggg aatcttaaaa aatagtcggc accattcccc cgtccatacg 2432

gatcggggac cttttaaatg cggatgcata gggactgcat acaaatgcag ccagtctgcc 2492

gatttcaata ggcttgataa atcgctgtat ttcggattga ggcagggtttg tcgtcataaa 2552

tttcttctct ttttctgaaa aagtcattccc ttcattcgggg tacattccct caatgatttg 2612

cttcacattc tcagagagcg tcggccccgg catgatcgta ttgactgtca cttctgttcc 2672

gattgttaat ttgataagc tttttgacaa tgataatagc attgattttg tcatacaata 2732

ctgaggcatc tggcctgaag gcatcatcgc ttcttcactt gcgataaaga tga 2785

<210> 38

<211> 594

<212> PRT

<213> Bacillus licheniformis

<400> 38

Met Lys Arg Leu Arg Met Arg Lys His Leu Leu Ile Ala Val Cys Thr
1 5 10 15

Leu Ala Leu Leu Leu Ser Ser Pro Ile Val Ser Asp Ala Ser Pro Ala
20 25 30

Thr Lys Pro Thr Thr Ala Asp Ser Pro Gln Ser Ser Gly Phe Phe Val
35 40 45

10294.000.ST25.txt

Asp His Tyr Lys Asn Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn
 50 55 60
 Pro Val Ile Gly Leu Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly
 65 70 75 80
 Lys Thr Trp Asn Thr Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala
 85 90 95
 Asn Ile Gln Lys Val Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu
 100 105 110
 Glu Asn Ala Ala Tyr Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile
 115 120 125
 Ile Asp Gly Leu Gly Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly
 130 135 140
 Ala Thr Thr Thr Ile Thr Ser Ile Pro Ala Asp Ala Ser Ile Arg Lys
 145 150 155 160
 Tyr Asn Asp Glu Gly Thr Asn Ser Gly Ser Thr Ser Ser Glu Leu Gly
 165 170 175
 Asn Val Val Ser Leu Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Ser
 180 185 190
 Asn Pro Ala Lys Ser Tyr Phe Asn Tyr Pro Arg Pro Phe Arg Trp Lys
 195 200 205
 Asp Asn Ser Ile Ile Val Pro Thr Leu Ile Pro Val Ile Asn Pro Asp
 210 215 220
 Pro Asn Lys Asp Gly Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr
 225 230 235 240
 Leu Ser Ala Phe Ala Met Ala Tyr Ala Ile Pro Glu Arg Tyr Gln Glu
 245 250 255
 Leu Leu Thr Arg Ala Ser Glu Leu Gly His Asn Arg Ile Val Ala Gly
 260 265 270
 Met His Ser Pro Leu Asp Val Met Gly Gly Arg Val Met Ala Thr Ala
 275 280 285
 Leu Ser Ala Ala Ile Leu Ser Asp Pro Ala Asn Glu Arg Leu Lys Lys
 290 295 300
 Thr Ala Phe Asp Glu Ala Arg Arg Lys Leu Leu Thr Gln Thr Gly Thr
 305 310 315 320

Ala Glu Asp Arg Tyr Ser Asp Tyr Glu Lys Asn Lys Lys Gln Tyr Thr
 325 330 335
 Glu Arg Leu Thr Tyr Gly Phe Arg Gln Met Asn Lys Thr Ala Lys Pro
 340 345 350
 Met Ala Val Pro Lys Gly Ala Glu Val Leu Leu Glu Thr Arg Phe Pro
 355 360 365
 Tyr Leu Asp Lys Lys Gln Arg Arg Ser Val Leu Ala Thr Thr Gly Leu
 370 375 380
 Pro Ala Gly Tyr Pro Val Leu Asp Asp Arg Glu Gly Trp Gly Arg Leu
 385 390 395 400
 Asn Leu Phe Ser Ala Ala Asp Gly Tyr Gly Ala Phe Thr Lys Asn Val
 405 410 415
 Thr Val Thr Met Asp Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg
 420 425 430
 Trp Arg Asn Asp Ile Ser Gly Thr Gly Lys Leu Thr Lys Lys Gly Thr
 435 440 445
 Gly Ala Leu Lys Leu Glu Gly Asp Asn Thr Tyr Ser Gly Gly Thr Arg
 450 455 460
 Ile Asp Gln Gly Thr Leu Glu Gly Gly Ser Glu Thr Ala Phe Gly Arg
 465 470 475 480
 Gly Asp Val Ala Leu Asn Gly Gly Ile Leu Lys Glu Asp Ala Pro Gly
 485 490 495
 Lys Leu Ile Ile Glu Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu
 500 505 510
 Glu Leu Gln Leu Ser Gly Lys Lys Asp Gln Leu Lys Ile Lys Gly Lys
 515 520 525
 Ala Arg Leu Lys Gly Thr Leu Arg Leu Asn Phe Thr Asp Asn Tyr Val
 530 535 540
 Pro Ala Asp Gly Ser Ala Ile Ile Thr Phe Arg Lys Arg His Gly Ser
 545 550 555 560
 Phe Ser Ser Val Glu Thr Ser Gly Leu Pro Ser Lys Tyr Lys Val Lys
 565 570 575
 Ile Ile Tyr Lys Ser Asn Ser Ile Gln Leu Lys Val Glu Gln Lys Gly
 580 585 590

Arg Ser

<210> 39

<211> 2009

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(1526)

<223>

<400> 39

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ccctgagcag cgcaaaaact gccggtcagc ggccgaaaac agcagagggtg aagttttctt	120
actttgttaa agaaaaatca aatgggctatg ttctatcaaa cggaaaaactt tcttaaaaaa	180
cagcgattat ttccgtgacg acgactcaat taagatcgat gctgggcggc atgaatatga	240
agagcacgta tgcttctgta tccagcaata cgaacgcttt tactctcagc ggtaaaggat	300
tcggacacgg catcggcatg agtcagtacg gatcaaatgc cagagctgct gccgggcacg	360
attacaagaa gattttaagt ttctactatc caaatacgac tctatcaagc tattaataga	420
gtttgaacag gaagcagcag tgcctcctct gttcatgttc atgggaaaac ataacattta	480
catttttgga gggtattttt ttg aag gtc ttt ctt aaa gct gta cct atg ttg	533
Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu	
1 5 10	
tcg tta cgg ttc ttt ttg ttt gtg cct aat gta ttt gcg gcc aac tct	581
Ser Leu Arg Phe Phe Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser	
15 20 25	
gtc aca aga ttg gac ggt gca aac cga tat gag gtt gcg gtg aac gtt	629
Val Thr Arg Leu Asp Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val	
30 35 40	
tcc aag cag ggg tgg aca agt gca agc act gtg att gtt gca aat gga	677
Ser Lys Gln Gly Trp Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly	
45 50 55	
aag gca tat gca gac gtc ctt tca gcg act cca ttt gcc tat cga aac	725
Lys Ala Tyr Ala Asp Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn	
60 65 70 75	
aac gcg cct gtt cta tta acg gaa gcg tct aaa ctg cca acg gcc act	773
Asn Ala Pro Val Leu Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr	
80 85 90	
aaa aac cga atc agt caa tta aaa cct agc aaa gtg atc gta atc ggc	821
Lys Asn Arg Ile Ser Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly	
95 100 105	

10294.000.ST25.txt

gga acc gtc agc gtt caa aac ggt gtc gta agc gag atc aaa aag ctt Gly Thr Val Ser Val Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu 110 115 120	869
ggt gtg tca tct gtc gaa cgc atc ggc gga gcg aat cgc tac gag gtt Gly Val Ser Ser Val Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val 125 130 135	917
gcg gcg aat att gcg aat aag ctg ccg agc aat tcg aaa gct gtc atc Ala Ala Asn Ile Ala Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile 140 145 150 155	965
gca aac ggg acg gcc tat gct gac agc ctt gcg atc ggc gca tat gcc Ala Asn Gly Thr Ala Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala 160 165 170	1013
gcg aga aac ggc atc ccg att ctt tta aca tcg tcg aat tcc ata ccg Ala Arg Asn Gly Ile Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro 175 180 185	1061
aca gcg aca aaa aat gcg atg aag agc aaa gga aca aca tcg acc att Thr Ala Thr Lys Asn Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile 190 195 200	1109
gtc gta ggc ggt gaa gtc agc atc tcc agc agc gtt tac aaa cag ctt Val Val Gly Gly Glu Val Ser Ile Ser Ser Val Tyr Lys Gln Leu 205 210 215	1157
gct tct ccg acg cgg atc ggc ggc agc aac cgc tat gaa gtc gcg gcc Ala Ser Pro Thr Arg Ile Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala 220 225 230 235	1205
aat gtc gtc aag aaa tat tat tct tct gcc aag aat gca atc atc agc Asn Val Val Lys Lys Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser 240 245 250	1253
aac ggc tat gcg tat gcc gac gga tta aca gga tct gtt ctg gcg gct Asn Gly Tyr Ala Tyr Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala 255 260 265	1301
aag caa aac cgt ccg atg atg ttc acg aat gca tca tct ttg ccg aca Lys Gln Asn Arg Pro Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr 270 275 280	1349
ccg aca aga gaa gtg atc ggt tcc aaa aac atg acg acg ttt act gtg Pro Thr Arg Glu Val Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val 285 290 295	1397
ctt ggc gga acg gtt tct ctt caa tcc aat gtc gtg tca cag ctg aag Leu Gly Gly Thr Val Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys 300 305 310 315	1445
aat ccg atc gtc gcc aaa aaa atc ttc att gat gca ggg cac gga ggt Asn Pro Ile Val Gly Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly 320 325 330	1493
aca gac agc ggt gcc cgt cgg caa cgg ttt ata tgagaaaagc gtgaaccttg Thr Asp Ser Gly Ala Arg Arg Gln Arg Phe Ile 335 340	1546
atgttgcaaa attaattaat acgaaactat caaacggcgg tgctctgccca attatggcga	1606
gaacgaacga cacttacctg acgctcgcac agcgcgtgtc aaaagcgcag tcaaatcatg	1666
cggatttggtt tgtcagcatc catgcaaact cggcaacgcc agctgcttcc ggaacagaaa	1726
cctactatta tacaacatat gaatctgccca acagcaaacg gctggcaacc gagattcaaa	1786

10294.000.ST25.txt

accgtctcta tgttgcatg aatacaaaaa accgcggtgt aaagatcggc aacttccatg 1846
tcatcagggga atcaaaaatg ccaagctgcc ttgttgaact tgcgtttatc agcaatgtaa 1906
gcgatgacgac aaaactcaaa agctcgactt acaaagaaaa aggcgctaaa gcgatttacg 1966
acggaatcgt tgcttactat taaaatataa acagaaaact cgt 2009

<210> 40

<211> 342

<212> PRT

<213> Bacillus licheniformis

<400> 40

Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu Ser Leu Arg Phe Phe
1 5 10 15

Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser Val Thr Arg Leu Asp
20 25 30

Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val Ser Lys Gln Gly Trp
35 40 45

Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly Lys Ala Tyr Ala Asp
50 55 60

Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn Asn Ala Pro Val Leu
65 70 75 80

Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr Lys Asn Arg Ile Ser
85 90 95

Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly Gly Thr Val Ser Val
100 105 110

Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu Gly Val Ser Ser Val
115 120 125

Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val Ala Ala Asn Ile Ala
130 135 140

Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile Ala Asn Gly Thr Ala
145 150 155 160

Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala Ala Arg Asn Gly Ile
165 170 175

Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro Thr Ala Thr Lys Asn
180 185 190

Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile Val Val Gly Gly Glu
 195 200 205

Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu Ala Ser Pro Thr Arg
 210 215 220

Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala Asn Val Val Lys Lys
 225 230 235 240

Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser Asn Gly Tyr Ala Tyr
 245 250 255

Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala Lys Gln Asn Arg Pro
 260 265 270

Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr Pro Thr Arg Glu Val
 275 280 285

Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val Leu Gly Gly Thr Val
 290 295 300

Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys Asn Pro Ile Val Gly
 305 310 315 320

Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly Thr Asp Ser Gly Ala
 325 330 335

Arg Arg Gln Arg Phe Ile
 340

<210> 41

<211> 2044

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (469)..(1566)

<223>

<400> 41

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ggcagcatca ccgaaatcgt caccgcgatt caaacgaaa catcttccat ggccggtgat 120

ttaaaaaccg gtttttcaga agttcataaa ggaaaaaacc agattgagac ttccggccga 180

10294.000.ST25.txt

tacttttcag agattaaaaa taaagtgcag gatatggctg gccgtgtatc ggacatttcg 240
gaggcattat cgcatttcag acgttcaagc gaggagatta acggctcggg cgagcatatc 300
gcggcgattt ccgaagaaaag cgcggccggg tctgaagaaa tttcagcgtc cgtacatgag 360
caaagcggct cgattgaaaa gatggacgaa agcgcaaggc ttctgggaga gatggttgaa 420
cggatgaatg tgatgatcaa acggtttaag ctctgatgcc gatacaga atg ggg ggt 477
Met Gly Gly
1

ttt aat gtt gtc gat ata tgt gaa aag agg gct gtt ggc act tgc gct 525
Phe Asn Val Val Asp Ile Cys Glu Lys Arg Ala Val Gly Thr Cys Ala
5 10 15

gtt cag tct cct cac agc tgt tgc cgg gtg ctc att caa ttc tgc tta 573
Val Gln Ser Pro His Ser Cys Cys Arg Val Leu Ile Gln Phe Cys Leu
20 25 30 35

aaa aag cgc caa ccg tta aga aaa agt aaa gct gat tgc cga ctc cga 621
Lys Lys Arg Gln Pro Leu Arg Lys Ser Lys Ala Asp Cys Arg Leu Arg
40 45 50

caa att gta cgt cgg ttt tgc cat cga tac gct gaa gga aga acg ctg 669
Gln Ile Val Arg Arg Phe Cys His Arg Tyr Ala Glu Gly Arg Thr Leu
55 60 65

gta caa aga tca aga agc gtt cga gaa aga agt tca aaa cct cgg ggg 717
Val Gln Arg Ser Arg Ser Val Arg Glu Arg Ser Ser Lys Pro Arg Gly
70 75 80

gga agt caa gac gct tgc cgc tca cgg aaa tca aga agt tca gat tca 765
Gly Ser Gln Asp Ala Cys Ser Arg Lys Ser Arg Ser Ser Asp Ser
85 90 95

gca ggc cga gct ctt gat cag cga agg cgt cga cgt gct tgt tgt tgt 813
Ala Gly Arg Ala Leu Asp Gln Arg Arg Arg Arg Arg Ala Cys Cys Cys
100 105 110 115

acc ggc aga tgc gga tgc cgc ggc gga gat cgt gaa aaa ggc gca cag 861
Thr Gly Arg Cys Gly Cys Arg Gly Gly Asp Arg Glu Lys Gly Ala Gln
120 125 130

cgc cgg tgt aaa agt gat ttc gta tta ccg gct gat tcg aaa cgc gga 909
Arg Arg Cys Lys Ser Asp Phe Val Leu Pro Ala Asp Ser Lys Arg Gly
135 140 145

tgt tta tta tta cgt ttc att tta tca cga aaa ggt cgg gga act gca 957
Cys Leu Leu Leu Arg Phe Ile Leu Ser Arg Lys Gly Arg Gly Thr Ala
150 155 160

ggc gga agc gat tgt aaa aaa agc gaa gaa agg aaa ctt cgt ata tat 1005
Gly Gly Ser Asp Cys Lys Lys Ser Glu Glu Arg Lys Leu Arg Ile Tyr
165 170 175

cgg cgg atc gtc tct tta caa caa tgc ggt ctt att ccg gaa cgg cgc 1053
Arg Arg Ile Val Ser Leu Gln Gln Cys Gly Leu Ile Pro Glu Arg Arg
180 185 190 195

cat gaa agt gct cga acc gtt gaa gcg gca ggg tca agt caa gct cgt 1101
His Glu Ser Ala Arg Thr Val Glu Ala Ala Gly Ser Ser Gln Ala Arg
200 205 210

gct tta cga ata tac gaa aga ctg gct acc aga aga agc gaa aaa gaa 1149
Ala Leu Arg Ile Tyr Glu Arg Leu Ala Thr Arg Arg Ser Glu Lys Glu
215 220 225

10294.000.ST25.txt

cat gaa aaa agc att gaa caa gac gag aga tat cga cgc cgt gat cgc His Glu Lys Ser Ile Glu Gln Asp Glu Arg Tyr Arg Arg Arg Asp Arg 230 235 240	1197
cgc caa tta cgg tac ggc tgg cgg ggt gat cga ggc gct tca gga ggc Arg Gln Leu Arg Tyr Gly Trp Arg Gly Asp Arg Gly Ala Ser Gly Gly 245 250 255	1245
ggg cct ggc cgg gaa aat tcc ggt gtc cgg aca gga cgc gga aat tca Gly Pro Gly Arg Glu Asn Ser Gly Val Arg Thr Gly Arg Gly Asn Ser 260 265 270	1293
agg cgt ccg acg aat tgt gaa cgg tac gca gac gat gac cgt tta caa Arg Arg Pro Thr Asn Cys Glu Arg Tyr Ala Asp Asp Asp Arg Leu Gln 280 285 290	1341
acc gat tcc cgc gct tgc caa aaa aag cgc tta aat ggc tgt tca agc Thr Asp Ser Arg Ala Cys Gln Lys Lys Arg Leu Asn Gly Cys Ser Ser 295 300 305	1389
ggc gaa agg cga agc gat tca aac cga tac aac cgt cga aaa cgg caa Gly Glu Arg Arg Ser Asp Ser Asn Arg Tyr Asn Arg Arg Lys Arg Gln 310 315 320	1437
agc caa agt acc ggc gat ttt act tta gcc gta tgc cgt tac gaa agg Ser Gln Ser Thr Gly Asp Phe Thr Leu Ala Val Cys Arg Tyr Glu Arg 325 330 335	1485
caa tat caa tta gac tgt gat caa aga cgg cca tct gtc caa aaa aga Gln Tyr Gln Leu Asp Cys Asp Gln Arg Arg Pro Ser Val Gln Lys Arg 340 345 350 355	1533
tat tca tca ata aaa cga agt cag cca tcc gct acaggatggc tgactttggt Tyr Ser Ser Ile Lys Arg Ser Gln Pro Ser Ala 360 365	1586
aaatttccac tttcacatcg gcgcttttct taagcttttc gacctgctgt ccgagttttt	1646
cctgtctttt ttgctgtttg agcatatctt ggatttgctg tttgacatcg tcaaacgcag	1706
gtgtgttttt ctgtccgctg tctttttgct gtgcggcaaa ttgatcataa tagtctttga	1766
tttctttgtc tgtaacctga tctgtcggca gttctttgtc aatatatttc tctgttttga	1826
tgctgtcggc aatgtcgctt ttcagcgtgt tcatgtttaa gcctgctttt ttgaccgctt	1886
cctcaaaatc ttgctcgttt ttatactgct ttttgctttc gtccagctgt ttttcaattt	1946
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<210> 42

<211> 366

<212> PRT

<213> Bacillus licheniformis

<400> 42

Met Gly Gly Phe Asn Val Val Asp Ile Cys Glu Lys Arg Ala Val Gly
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Thr Cys Ala Val Gln Ser Pro His Ser Cys Cys Arg Val Leu Ile Gln
 20 25 30
 Phe Cys Leu Lys Lys Arg Gln Pro Leu Arg Lys Ser Lys Ala Asp Cys
 35 40 45
 Arg Leu Arg Gln Ile Val Arg Arg Phe Cys His Arg Tyr Ala Glu Gly
 50 55 60
 Arg Thr Leu Val Gln Arg Ser Arg Ser Val Arg Glu Arg Ser Ser Lys
 65 70 75 80
 Pro Arg Gly Gly Ser Gln Asp Ala Cys Arg Ser Arg Lys Ser Arg Ser
 85 90 95
 Ser Asp Ser Ala Gly Arg Ala Leu Asp Gln Arg Arg Arg Arg Ala
 100 105 110
 Cys Cys Cys Thr Gly Arg Cys Gly Cys Arg Gly Gly Asp Arg Glu Lys
 115 120 125
 Gly Ala Gln Arg Arg Cys Lys Ser Asp Phe Val Leu Pro Ala Asp Ser
 130 135 140
 Lys Arg Gly Cys Leu Leu Leu Arg Phe Ile Leu Ser Arg Lys Gly Arg
 145 150 155 160
 Gly Thr Ala Gly Gly Ser Asp Cys Lys Lys Ser Glu Glu Arg Lys Leu
 165 170 175
 Arg Ile Tyr Arg Arg Ile Val Ser Leu Gln Gln Cys Gly Leu Ile Pro
 180 185 190
 Glu Arg Arg His Glu Ser Ala Arg Thr Val Glu Ala Ala Gly Ser Ser
 195 200 205
 Gln Ala Arg Ala Leu Arg Ile Tyr Glu Arg Leu Ala Thr Arg Arg Ser
 210 215 220
 Glu Lys Glu His Glu Lys Ser Ile Glu Gln Asp Glu Arg Tyr Arg Arg
 225 230 235 240
 Arg Asp Arg Arg Gln Leu Arg Tyr Gly Trp Arg Gly Asp Arg Gly Ala
 245 250 255
 Ser Gly Gly Gly Pro Gly Arg Glu Asn Ser Gly Val Arg Thr Gly Arg
 260 265 270
 Gly Asn Ser Arg Arg Pro Thr Asn Cys Glu Arg Tyr Ala Asp Asp Asp
 275 280 285

10294.000.ST25.txt

Arg Leu Gln Thr Asp Ser Arg Ala Cys Gln Lys Lys Arg Leu Asn Gly
 290 295 300
 Cys Ser Ser Gly Glu Arg Arg Ser Asp Ser Asn Arg Tyr Asn Arg Arg
 305 310 315 320
 Lys Arg Gln Ser Gln Ser Thr Gly Asp Phe Thr Leu Ala Val Cys Arg
 325 330 335
 Tyr Glu Arg Gln Tyr Gln Leu Asp Cys Asp Gln Arg Arg Pro Ser Val
 340 345 350
 Gln Lys Arg Tyr Ser Ser Ile Lys Arg Ser Gln Pro Ser Ala
 355 360 365

<210> 43
 <211> 1690
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (480)..(1208)
 <223>

<400> 43
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 cccgcaggcg acattgctga tcctcggtgt ggcaagggag ttgtccgcca atgtcagtgc 180
 atcgattccg gctgatttta gtcctctgc ggcggtgcaaa aatttctcaa agtttaattg 240
 ttttggagga tcgagctcga cgataatgga ccgtttctgc ttagccagat agtcaagagc 300
 aggctatgtc ctttcgtttt ggacggcaag cgccgctttc tttgggattt tcactagttt 360
 ttcggtgact ggaggaagtt ctttgacggc cctcggcatc gttctaccct gagtgtcttt 420
 tatgcccgtc tttaggcggc cccgtcaacg aataatgcat aaaaaaggaa gattcatat 479
 gaa aat cgt aaa cgt tct gct cgc tat ttt att gac cgc aat cat gtt 527
 Glu Asn Arg Lys Arg Ser Ala Arg Tyr Phe Ile Asp Arg Asn His Val
 1 5 10 15
 aag cgg ttg ttt gta ccc tta aga aag aaa ggc gaa aaa cag cgc acc 575
 Lys Arg Leu Phe Val Pro Leu Arg Lys Lys Gly Glu Lys Gln Arg Thr
 20 25 30
 gca tca gca cca gct caa aga agt gca ggc ggc cgt tta tta att cag 623
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Ala Ser Ala Pro Ala Gln Arg Ser Ala Gly Gly Arg Leu Leu Ile Gln
35 40 45

gga ggc gac ggg agg gct tct gcc gat tca gac aag gga tat ggg cgt 671
Gly Gly Asp Gly Arg Ala Ser Ala Asp Ser Asp Lys Gly Tyr Gly Arg
50 55 60

gcc aat cta tca aaa ata ccc tat cga ttt tca cag gct gtc ccc ccg 719
Ala Asn Leu Ser Lys Ile Pro Tyr Arg Phe Ser Gln Ala Val Pro Pro
65 70 75 80

gta tat ggc tta gcc gcc ggg cac atc cta tta aaa cgg cgg aga gta 767
Val Tyr Gly Leu Ala Ala Gly His Ile Leu Leu Lys Arg Arg Arg Val
85 90 95

ctt gta cgt tct tgt cga tgt gga aaa aaa gcc gac ggt caa gct cat 815
Leu Val Arg Ser Cys Arg Cys Gly Lys Lys Ala Asp Gly Gln Ala His
100 105 110

tta tgt aaa aat gtc gga aat gat cag gga gtt aaa gct tcg ggt cga 863
Leu Cys Lys Asn Val Gly Asn Asp Gln Gly Val Lys Ala Ser Gly Arg
115 120 125

aat gta tca aga tca gca caa gta tcc gcc gta tca aaa agt cgt atc 911
Asn Val Ser Arg Ser Ala Gln Val Ser Ala Val Ser Lys Ser Arg Ile
130 135 140

caa gaa ctt att cat gct tta cca tta aaa gct cgg act gaa aga ggc 959
Gln Glu Leu Ile His Ala Leu Pro Leu Lys Ala Arg Thr Glu Arg Gly
145 150 155 160

gcc ttc tgt cac gag tcc gct ttc ggg cac ctc gct gcc gct tct cgt 1007
Ala Phe Cys His Glu Ser Ala Phe Gly His Leu Ala Ala Ala Ser Arg
165 170 175

cga tta aaa agg cga cat tca agt gga tta ccg gat gga ttt ggc caa 1055
Arg Leu Lys Arg Arg His Ser Ser Gly Leu Pro Asp Gly Phe Gly Gln
180 185 190

gct gat gaa gaa gtc gaa aaa aac ggt aaa gcc ggg cga gga agt cca 1103
Ala Asp Glu Glu Val Glu Lys Asn Gly Lys Ala Gly Arg Gly Ser Pro
195 200 205

aga ttt gat gtg gga aga gac gcc ttt cgt tcc ggc gtt ttc ggt aaa 1151
Arg Phe Asp Val Gly Arg Asp Ala Phe Arg Ser Gly Val Phe Gly Lys
210 215 220

gta cac agt gaa tta caa aca gga acc tgt ttt tct cga ata gaa tat 1199
Val His Ser Glu Leu Gln Thr Gly Thr Cys Phe Ser Arg Ile Glu Tyr
225 230 235 240

cgg tca aaa tgcaagtatc agtcatgaac ctttctcctc ggcataacaat 1248
Arg Ser Lys

gaggagaaag gttttttcat gtatgccgaa aaaatttccc taagctgtca tattgaaata 1308

ggacaacgtc atacactata gtgtcctggt tttgattgat gaagaagtaa aaaattgaaa 1368

aggattggaa gtccggagg ggatcacttg gaaaaggctg atattttcaa ggatatcgct 1428

gaacgaacag gaggcgatat atacttaggt gtcgtaggag ctgtacgtac aggaaaatct 1488

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<211> 243

<212> PRT

<213> Bacillus licheniformis

<400> 44

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 20 25 30
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 35 40 45
 Gly Gly Asp Gly Arg Ala Ser Ala Asp Ser Asp Lys Gly Tyr Gly Arg
 50 55 60
 Ala Asn Leu Ser Lys Ile Pro Tyr Arg Phe Ser Gln Ala Val Pro Pro
 65 70 75 80
 Val Tyr Gly Leu Ala Ala Gly His Ile Leu Leu Lys Arg Arg Arg Val
 85 90 95
 Leu Val Arg Ser Cys Arg Cys Gly Lys Lys Ala Asp Gly Gln Ala His
 100 105 110
 Leu Cys Lys Asn Val Gly Asn Asp Gln Gly Val Lys Ala Ser Gly Arg
 115 120 125
 Asn Val Ser Arg Ser Ala Gln Val Ser Ala Val Ser Lys Ser Arg Ile
 130 135 140
 Gln Glu Leu Ile His Ala Leu Pro Leu Lys Ala Arg Thr Glu Arg Gly
 145 150 155 160
 Ala Phe Cys His Glu Ser Ala Phe Gly His Leu Ala Ala Ala Ser Arg
 165 170 175
 Arg Leu Lys Arg Arg His Ser Ser Gly Leu Pro Asp Gly Phe Gly Gln
 180 185 190
 Ala Asp Glu Glu Val Glu Lys Asn Gly Lys Ala Gly Arg Gly Ser Pro
 195 200 205

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Arg Phe Asp Val Gly Arg Asp Ala Phe Arg Ser Gly Val Phe Gly Lys
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Val His Ser Glu Leu Gln Thr Gly Thr Cys Phe Ser Arg Ile Glu Tyr
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Arg Ser Lys

<210> 45

<211> 1759

<212> DNA

<213> Bacillus Ticheniformis

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<222> (476)..(1267)

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 ccgtcctgtc attatatgta agtcgaagct tgcattgtgcc tactggaagg gcgcattctc 360
 gacatgtggc aaaatgggtg ggggagagcg caatctatct taaaaaatg aagtttgacg 420
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 Leu
 1

aaa aag gca ata ttg acg gtc ata gct gta ttg acg tcg gtt gtt ttg 526
 Lys Lys Ala Ile Leu Thr Val Ile Ala Val Leu Thr Ser Val Val Leu
 5 10 15

ttc gcc ggc tgc caa gcg gaa aaa ggg gga tca gcc aag ggg cag tct 574
 Phe Ala Gly Cys Gln Ala Glu Lys Gly Gly Ser Ala Lys Gly Gln Ser
 20 25 30

gaa aaa gtt caa att acg gtt tcc gcg gct gcg agt ctc aag gat gtt 622
 Glu Lys Val Gln Ile Thr Val Ser Ala Ala Ala Ser Leu Lys Asp Val
 35 40 45

tta aca gaa ctt tcc tcc gtc tat gag aaa gac cat ccg aat gtc tct 670
 Leu Thr Glu Leu Ser Ser Val Tyr Glu Lys Asp His Pro Asn Val Ser
 50 55 60 65

ata aag ttt aat ttt ggt tca tcg ggt gca ttg cag cag cag atc gaa 718

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Gln	Gly	Ala	Pro	Ala	Asp	Leu	Phe	Phe	Ser	Ala	Ala	Glu	Asp	Lys	Phe	
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aat	aga	gta	gtt	gat	caa	ggg	tta	att	gac	aaa	aaa	gac	tct	gtc	aag	814
Asn	Arg	Val	Val	Asp	Gln	Gly	Leu	Ile	Asp	Lys	Lys	Asp	Ser	Val	Lys	
		100					105					110				
ctg	gtc	gaa	aac	agt	ctg	gtg	ctg	atc	gtg	ccg	aaa	gga	aaa	agt	cag	862
Leu	Val	Glu	Asn	Ser	Leu	Val	Leu	Ile	Val	Pro	Lys	Gly	Lys	Ser	Gln	
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cat	gtc	aac	agc	ttc	aag	gat	ttg	gcg	gat	gac	aaa	gtc	gaa	aaa	att	910
His	Val	Asn	Ser	Phe	Lys	Asp	Leu	Ala	Asp	Asp	Lys	Val	Glu	Lys	Ile	
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Ala	Ile	Gly	Lys	Pro	Glu	Ser	Val	Pro	Ala	Gly	Lys	Tyr	Ala	Lys	Glu	
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acg	ttg	acg	aac	ctt	gac	gta	tgg	tct	aaa	gtg	caa	tct	aaa	gtc	gtc	1006
Thr	Leu	Thr	Asn	Leu	Asp	Val	Trp	Ser	Lys	Val	Gln	Ser	Lys	Val	Val	
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tac	agc	aaa	gat	gta	agg	cag	gtc	ctt	tct	tat	atc	gaa	aca	ggc	aac	1054
Tyr	Ser	Lys	Asp	Val	Arg	Gln	Val	Leu	Ser	Tyr	Ile	Glu	Thr	Gly	Asn	
		180					185					190				
gcg	gat	gcc	gga	atc	gtt	tac	cgg	acg	gac	gcc	ctt	tca	tca	gat	cag	1102
Ala	Asp	Ala	Gly	Ile	Val	Tyr	Arg	Thr	Asp	Ala	Leu	Ser	Ser	Asp	Gln	
	195					200					205					
gtc	gag	acc	gta	gag	acg	gcg	aaa	agc	gat	ctg	cat	aca	ccg	att	gtc	1150
Val	Glu	Thr	Val	Glu	Thr	Ala	Lys	Ser	Asp	Leu	His	Thr	Pro	Ile	Val	
	210				215					220					225	
tat	ccg	ctc	gga	att	gtg	aaa	aat	aca	aag	cac	agg	gaa	cag	tct	gag	1198
Tyr	Pro	Leu	Gly	Ile	Val	Lys	Asn	Thr	Lys	His	Arg	Glu	Gln	Ser	Glu	
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gaa	ttt	tat	caa	ttc	ctg	caa	agc	gac	caa	gcc	gtc	aag	gcg	atg	gaa	1246
Glu	Phe	Tyr	Gln	Phe	Leu	Gln	Ser	Asp	Gln	Ala	Val	Lys	Ala	Met	Glu	
			245					250					255			
aag	tac	gga	ttt	aag	aag	ggc	tgaccg	ccgt	tatgcttgag	gagttcttat						1297
Lys	Tyr	Gly	Phe	Lys	Lys	Gly										
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acggagcaaa	cgaatggagg	gtgttcctct	ttgtcaccgt	tccccttgca	tccaatggaa											1717
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<210> 46

<211> 264

<212> PRT

<213> Bacillus licheniformis

<400> 46

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 20 25 30

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 35 40 45

Val Leu Thr Glu Leu Ser Ser Val Tyr Glu Lys Asp His Pro Asn Val
 50 55 60

Ser Ile Lys Phe Asn Phe Gly Ser Ser Gly Ala Leu Gln Gln Gln Ile
 65 70 75 80

Glu Gln Gly Ala Pro Ala Asp Leu Phe Phe Ser Ala Ala Glu Asp Lys
 85 90 95

Phe Asn Arg Val Val Asp Gln Gly Leu Ile Asp Lys Lys Asp Ser Val
 100 105 110

Lys Leu Val Glu Asn Ser Leu Val Leu Ile Val Pro Lys Gly Lys Ser
 115 120 125

Gln His Val Asn Ser Phe Lys Asp Leu Ala Asp Asp Lys Val Glu Lys
 130 135 140

Ile Ala Ile Gly Lys Pro Glu Ser Val Pro Ala Gly Lys Tyr Ala Lys
 145 150 155 160

Glu Thr Leu Thr Asn Leu Asp Val Trp Ser Lys Val Gln Ser Lys Val
 165 170 175

Val Tyr Ser Lys Asp Val Arg Gln Val Leu Ser Tyr Ile Glu Thr Gly
 180 185 190

Asn Ala Asp Ala Gly Ile Val Tyr Arg Thr Asp Ala Leu Ser Ser Asp
 195 200 205

Gln Val Glu Thr Val Glu Thr Ala Lys Ser Asp Leu His Thr Pro Ile
 210 215 220

Val Tyr Pro Leu Gly Ile Val Lys Asn Thr Lys His Arg Glu Gln Ser
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Glu Glu Phe Tyr Gln Phe Leu Gln Ser Asp Gln Ala Val Lys Ala Met
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<210> 47

<211> 2449

<212> DNA

<213> Bacillus licheniformis

<220>

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<222> (501)..(1946)

<223>

<400> 47

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ccgcagttag gagggatgat tgggaacggt catgttgtca gaagcaatct attacatatt 480
gaaaaagggg ggaaatattg atg aac atc aaa aac att gct aaa aaa gcg tca 533
Met Asn Ile Lys Asn Ile Ala Lys Lys Ala Ser
1 5 10

gcc tta acc gtt gct gcg gca ctg ctg gcc gga ggt gcg ccg caa acc 581
Ala Leu Thr Val Ala Ala Ala Leu Leu Ala Gly Gly Ala Pro Gln Thr
15 20 25

ttt gca aaa gaa acg cag gat tac aag aaa agc tac gga ttt tct cat 629
Phe Ala Lys Glu Thr Gln Asp Tyr Lys Lys Ser Tyr Gly Phe Ser His
30 35 40

atc aca aga cat gac atg ctg aaa att ccc gag cag caa aag agc gaa 677
Ile Thr Arg His Asp Met Leu Lys Ile Pro Glu Gln Gln Lys Ser Glu
45 50 55

caa ttt aaa gtt cct caa ttc gat ccg aaa aca atc aaa aac atc cct 725
Gln Phe Lys Val Pro Gln Phe Asp Pro Lys Thr Ile Lys Asn Ile Pro
60 65 70 75

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tct gca aaa ggg tat aac aaa aat gga gag ctg atc gat tta gac gta Ser Ala Lys Gly Tyr Asn Lys Asn Gly Glu Leu Ile Asp Leu Asp Val 80 85 90	773
tgg gac agc tgg ccg ctg caa aat gcc gac ggg acg gtt gct aca tac Trp Asp Ser Trp Pro Leu Gln Asn Ala Asp Gly Thr Val Ala Thr Tyr 95 100 105	821
cac ggc tac aat ctt gtt ttc gcg ctg gcg ggc gat ccg aaa gac gtc His Gly Tyr Asn Leu Val Phe Ala Leu Ala Gly Asp Pro Lys Asp Val 110 115 120	869
gat gac aca tcc atc tat ttg ttc tat caa aag aaa ggc gaa act tct Asp Asp Thr Ser Ile Tyr Leu Phe Tyr Gln Lys Lys Gly Glu Thr Ser 125 130 135	917
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ttt gtt cca gac gat ccg tac ctc aaa cat caa aca cag gaa tgg tca Phe Val Pro Asp Asp Pro Tyr Leu Lys His Gln Thr Gln Glu Trp Ser 160 165 170	1013
ggt tct gcc acg ctg aca aaa gac gga aaa gtc cga ctg ttt tac aca Gly Ser Ala Thr Leu Thr Lys Asp Gly Lys Val Arg Leu Phe Tyr Thr 175 180 185	1061
gct ttt tcc ggc acg caa tac ggc aag cag acg ctg aca aca gct cag Ala Phe Ser Gly Thr Gln Tyr Gly Lys Gln Thr Leu Thr Ala Gln 190 195 200	1109
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gaa gat cat aaa tcg gtc ttt gac ggc gcc gac ggc acg gta tac caa Glu Asp His Lys Ser Val Phe Asp Gly Ala Asp Gly Thr Val Tyr Gln 220 225 230 235	1205
aac gtt cag caa ttc att gac gaa gga aac tac agc tcc ggc gac aac Asn Val Gln Gln Phe Ile Asp Glu Gly Asn Tyr Ser Ser Gly Asp Asn 240 245 250	1253
cat acg atg aga gac ccg cat tat gtg gaa gac cgc ggc cat aaa tat His Thr Met Arg Asp Pro His Tyr Val Glu Asp Arg Gly His Lys Tyr 255 260 265	1301
ctc gta ttt gaa gcc aat acg gga aca aaa acc ggc tac caa gga gaa Leu Val Phe Glu Ala Asn Thr Gly Thr Lys Thr Gly Tyr Gln Gly Glu 270 275 280	1349
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cca ttc aag cct tta aac aaa tcc gga ctt gtt ttg cat atg gac cag Pro Phe Lys Pro Leu Asn Lys Ser Gly Leu Val Leu His Met Asp Gln 400 405 410	1733
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tggagaatat cattactact acctctataa ccgagactat ccggacggca atggaacaga	2276
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<211> 482

<212> PRT

<213> Bacillus licheniformis

<400> 48

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 Gln Asp Tyr₃₅ Lys Lys Ser Tyr Gly₄₀ Phe Ser His Ile Thr₄₅ Arg His Asp
 Met Leu₅₀ Lys Ile Pro Glu Gln₅₅ Gln Lys Ser Glu Gln₆₀ Phe Lys Val Pro
 Gln Phe Asp Pro Lys Thr₇₀ Ile Lys Asn Ile Pro₇₅ Ser Ala Lys Gly Tyr₈₀
 Asn Lys Asn Gly Glu₈₅ Leu Ile Asp Leu Asp₉₀ Val Trp Asp Ser Trp₉₅ Pro
 Leu Gln Asn Ala₁₀₀ Asp Gly Thr Val Ala₁₀₅ Thr Tyr His Gly Tyr Asn Leu
 Val Phe Ala₁₁₅ Leu Ala Gly Asp Pro₁₂₀ Lys Asp Val Asp Asp₁₂₅ Thr Ser Ile
 Tyr Leu₁₃₀ Phe Tyr Gln Lys Lys₁₃₅ Gly Glu Thr Ser Ile₁₄₀ Asp Ser Trp Lys
 Asn Ala Gly Arg Val Phe₁₅₀ Lys Asp Ser Asp Lys₁₅₅ Phe Val Pro Asp Asp₁₆₀
 Pro Tyr Leu Lys His₁₆₅ Gln Thr Gln Glu Trp₁₇₀ Ser Gly Ser Ala Thr Leu₁₇₅
 Thr Lys Asp Gly₁₈₀ Lys Val Arg Leu Phe₁₈₅ Tyr Thr Ala Phe Ser₁₉₀ Gly Thr
 Gln Tyr Gly₁₉₅ Lys Gln Thr Leu Thr₂₀₀ Thr Ala Gln Val Asn₂₀₅ Phe Ser Gln
 Pro Asp₂₁₀ Ser Asp Thr Leu Lys₂₁₅ Ile Asp Gly Val Glu₂₂₀ Asp His Lys Ser
 Val Phe Asp Gly Ala Asp₂₃₀ Gly Thr Val Tyr Gln₂₃₅ Asn Val Gln Gln Phe₂₄₀
 Ile Asp Glu Gly Asn₂₄₅ Tyr Ser Ser Gly Asp₂₅₀ Asn His Thr Met Arg₂₅₅ Asp
 Pro His Tyr Val₂₆₀ Glu Asp Arg Gly His₂₆₅ Lys Tyr Leu Val Phe₂₇₀ Glu Ala
 Asn Thr Gly₂₇₅ Thr Lys Thr Gly Tyr₂₈₀ Gln Gly Glu Asp Ser₂₈₅ Leu Phe Asn

Arg Ala Tyr Tyr Gly Gly Ser Lys Lys Phe Phe Lys Glu Glu Ser Ser
 290 295 300

Lys Leu Leu Gln Gly Ala Asn Lys Lys Asn Ala Ser Leu Ala Asn Gly
 305 310 315 320

Ala Leu Gly Ile Ile Glu Leu Asn Asn Asp Tyr Thr Leu Lys Lys Val
 325 330 335

Met Lys Pro Leu Ile Ala Ser Asn Thr Val Thr Asp Glu Ile Glu Arg
 340 345 350

Ala Asn Leu Phe Lys Met Asn Gly Lys Trp Tyr Leu Phe Thr Asp Ser
 355 360 365

Arg Gly Ser Lys Met Thr Ile Asp Gly Ile Gly Ser Lys Asp Ile Tyr
 370 375 380

Met Leu Gly Tyr Val Ser Gly Ser Leu Thr Gly Pro Phe Lys Pro Leu
 385 390 395 400

Asn Lys Ser Gly Leu Val Leu His Met Asp Gln Asp Tyr Asn Asp Ile
 405 410 415

Thr Phe Thr Tyr Ser His Phe Ala Val Pro Gln Lys Lys Gly Asp Glu
 420 425 430

Val Val Ile Thr Ser Tyr Ile Thr Asn Arg Gly Ile Ser Asn Glu His
 435 440 445

His Ala Thr Phe Ala Pro Ser Phe Leu Leu Lys Ile Lys Gly Ser Lys
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Thr Ser Val Val Lys Asn Ser Ile Leu Glu Gln Gly Gln Leu Thr Val
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Asn Lys

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<211> 1669

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<223>

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 Gln Asp Ala Lys Gly Thr Ile Arg Ala Lys Asp Thr Gly Val Lys Tyr 205
 195 200
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Ser Asp Lys Asp Lys Glu Ser Ala Ser Asp Glu Asp Lys Ser Thr Ser
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 180 185 190

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420

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255

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Glu Lys Asn Ala Arg Val Pro Met Leu Ile Met Ala Ile His Gly Gly
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Ile Met Asn Ala Thr Asp Gln Ala Leu Lys Asp Tyr Asp Leu Ser Lys
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Trp Thr Val Thr Ser Gly Ser Ser Ser Ala Met Thr Ala Ala Leu Lys
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Lys Ala Tyr Asp Lys Lys Asp Pro Ile Ile Ile Thr Gly Trp Thr Pro
 85 90 95

His Trp Met Phe Ala Lys Tyr Asp Leu Lys Tyr Leu Lys Asp Pro Lys
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Gly Ser Tyr Gly Asp Ala Glu Glu Ile His Thr Val Thr Arg Lys Gly
 115 120 125

Phe Lys Asp Asp His Pro Gly Ala Asn Lys Leu Leu Ser Gln Phe Ser
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Ser Arg Ser Arg Pro Asp Val Ser Trp His Ala Lys Trp Lys Arg Arg
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<222> (501)..(1181)

<223>

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 gccatcagca ttgccaagcg gacgaggacg attgtctggc agaattattat ttttgcactc 240
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 gtgaaagaaa tgtaactttt ttaccaccta atgaactgga aattcctttt ttagcatctt 420
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Gly Val Lys Ile Asp Lys Pro Phe Asp Tyr Asp Lys Ile Lys Glu Thr
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 Lys Phe His Glu Ala Leu Tyr Lys Ala Gln Pro Asp Asn Asp Thr Met
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<211> 1856

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<222> (465)..(1358)

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Glu	Arg	Ile	Pro	Thr	Phe	Glu	Glu	Val	Leu	Asp	Arg	Tyr	Lys	Gly	Lys	
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gtc	gga	atg	ctg	atc	gaa	ttg	aaa	gag	cct	gca	cgc	tat	ccg	gga	atc	956
Val	Gly	Met	Leu	Ile	Glu	Leu	Lys	Glu	Pro	Ala	Arg	Tyr	Pro	Gly	Ile	
	150				155						160					
gaa	gga	aaa	gtg	tca	gca	gca	ttg	aaa	gag	cgg	aga	atg	gat	aag	cct	1004
Glu	Gly	Lys	Val	Ser	Ala	Ala	Leu	Lys	Glu	Arg	Arg	Met	Asp	Lys	Pro	
165					170					175					180	
aaa	aac	gga	aaa	atc	att	gta	caa	tcg	ttt	gat	ttt	aac	tct	gtc	tat	1052
Lys	Asn	Gly	Lys	Ile	Ile	Val	Gln	Ser	Phe	Asp	Phe	Asn	Ser	Val	Tyr	
				185					190					195		
aaa	att	cat	cag	ctg	ctt	cca	tcg	atg	ccg	aca	ggt	gtc	ttg	acg	tca	1100
Lys	Ile	His	Gln	Leu	Leu	Pro	Ser	Met	Pro	Thr	Gly	Val	Leu	Thr	Ser	
			200				205						210			
aaa	gcg	gcg	gac	tta	aca	gat	gca	aag	ctt	aag	gaa	ttt	tcc	ggc	tat	1148
Lys	Ala	Ala	Asp	Leu	Thr	Asp	Ala	Lys	Leu	Lys	Glu	Phe	Ser	Gly	Tyr	
		215					220					225				
gcc	aaa	tac	gtg	aac	gcc	aac	ttg	aaa	aat	gtg	gcc	gct	gat	cct	acg	1196
Ala	Lys	Tyr	Val	Asn	Ala	Asn	Leu	Lys	Asn	Val	Ala	Ala	Asp	Pro	Thr	
	230				235						240					
ctt	gtg	ccg	aga	att	cat	gcg	ctc	ggc	atg	aag	ata	cgc	cct	tgg	acc	1244
Leu	Val	Pro	Arg	Ile	His	Ala	Leu	Gly	Met	Lys	Ile	Arg	Pro	Trp	Thr	
245					250				255					260		
gtc	cgc	tcc	cgc	gat	gaa	gtg	cct	ccg	cta	tca	agg	ccc	gcg	tgg	aac	1292

10294.000.ST25.txt

Val Arg Ser Arg Asp Glu Val Pro Pro Leu Ser Arg Pro Ala Trp Asn
 265 270 275

ggg att gtg aca aaa ctt tcc cga cta ttg ttc caa aaa agt acg gga 1340
 Gly Ile Val Thr Lys Leu Ser Arg Leu Leu Phe Gln Lys Ser Thr Gly
 280 285 290

gcc cca ata aaa aac cct gaagtttgct ttgaagggt ttttaattta 1388
 Ala Pro Ile Lys Asn Pro
 295

aaaataaaaa tggggcttaa aacaaaaaag gttaacgtta acgggtttat cgttcccccc 1448
 gattttttttt gggacacctg ggaaaaacgg gtataaacct ttggggggccc tttttggggg 1508
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 aaaaaaaccc ggggggttttt ttttttgggt actgccgccg atgaccttac atatgggctg 1688
 aactgcaaaa acaatggaag aggaaaacct gcaggccgc atcgtctcat tcagcgttga 1748
 tcccgaaaat gatacgctg aaaaattgaa gaaatttgcg gccaaactacc cgctcagttt 1808
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<211> 298

<212> PRT

<213> Bacillus licheniformis

<400> 64

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Ser Leu Ile Gly Val Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala
 20 25 30

Gly Ala Gln Glu Pro Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala
 35 40 45

His Arg Gly Ala Ser Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe
 50 55 60

Asp Lys Ala Leu Gln Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln
 65 70 75 80

Met Ser Lys Asp Gly Glu Leu Val Ile Ile His Asp Thr Thr Val Asn
 85 90 95

Arg Thr Thr Asp Ile Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu
 100 105 110

10294.000.ST25.txt

Thr Leu Ala Glu Leu Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro
115 120 125

Gln Phe Ala Gly Glu Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg
130 135 140

Tyr Lys Gly Lys Val Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg
145 150 155 160

Tyr Pro Gly Ile Glu Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg
165 170 175

Met Asp Lys Pro Lys Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe
180 185 190

Asn Ser Val Tyr Lys Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly
195 200 205

Val Leu Thr Ser Lys Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu
210 215 220

Phe Ser Gly Tyr Ala Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala
225 230 235 240

Ala Asp Pro Thr Leu Val Pro Arg Ile His Ala Leu Gly Met Lys Ile
245 250 255

Arg Pro Trp Thr Val Arg Ser Arg Asp Glu Val Pro Pro Leu Ser Arg
260 265 270

Pro Ala Trp Asn Gly Ile Val Thr Lys Leu Ser Arg Leu Leu Phe Gln
275 280 285

Lys Ser Thr Gly Ala Pro Ile Lys Asn Pro
290 295

<210> 65

<211> 1768

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1265)

<223>

[illegible]

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 Thr Tyr Met Asn Gly Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu
 205 210 215
 tac atc aga acg acc gtc aca aaa cag aga aaa ccg tcc aat aat aaa 1205
 Tyr Ile Arg Thr Thr Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys
 220 225 230 235
 agc tca ggc ggc gga acg acg agc gga ggc cat tcg cac agc ggc agc 1253
 Ser Ser Gly Gly Gly Thr Thr Ser Gly Gly His Ser His Ser Gly Ser
 240 245 250
 cgg gga agc ttt tagaaaggga aaggaagagc ttaaattggtg ttttttagaa 1305
 Arg Gly Ser Phe
 255
 atcaatttgc aaatgtagta gagtgggatg aatttcgcga tgatatgatt ttctataaat 1365
 ggaacaaccg cgaaatcaaa aaggggagcc ggctgatcat tcgccccggt caggatgccg 1425
 tcttttttaa caacggaaaa attgaaggca ttttccagga tgagggcgac tatgatattg 1485
 aatccgaaat tattcctttt ttatccactt taaaaggttt taaatttggc tttacagcg 1545
 ggatgcgcgc cgaagtcctg tttgtcaaca cgaaggaatt taccgtcaag tgggggacga 1605
 agaatgccat caatatcccc gctgcaggac ttccgggcgg catgccgatc agggcgaacg 1665
 gaagatttaa ctttaagggtg aatgattatg tcgcattaat cgataaaatt gccggtgtga 1725
 aagatcagta tgttgtggaa gatatcaaaa tacggatcac atc 1768

<210> 66

<211> 255

<212> PRT

<213> Bacillus licheniformis

<400> 66

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 1 5 10 15
 Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala Ser Glu Gln Lys Arg
 20 25 30
 Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys Gln Glu Ile Glu Lys
 35 40 45
 Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu Arg Glu Thr Asp Phe
 50 55 60
 Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg Asp Val Lys Lys Tyr
 65 70 75 80
 Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly Tyr Gln Lys Lys His
 85 90 95

10294.000.ST25.txt

Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu His Arg Glu Val Tyr
100 105 110
Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu Asn Asp Ala Arg Leu
115 120 125
Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile Ser Asp Lys His Tyr
130 135 140
Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala His Asp Asp Met Glu
145 150 155 160
Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys Thr Trp Phe Gln Leu
165 170 175
Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val Ala Ile Met Lys Tyr
180 185 190
Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser Thr Tyr Met Asn Gly
195 200 205
Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu Tyr Ile Arg Thr Thr
210 215 220
Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys Ser Ser Gly Gly Gly
225 230 235 240
Thr Thr Ser Gly Gly His Ser His Ser Gly Ser Arg Gly Ser Phe
245 250 255

<210> 67

<211> 2206

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1703)

<223>

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gttccaaatg ctgccttggt gtatgttttg gcgtgtgtgt agacggtatt aaaaaagtga 180

10294.000.ST25.txt

aatatacctg taaaggagaa ttccccgagca tcctgagcag ctgtgtctcg gtcttgattt 240
tctgcggcat cagattaaga atcacaatat ttaaaggctct gatgtcctga tgaaaagccc 300
gtttttcatc catgacaaaa atatttttcac tttcaagaat ctgctttgct ggcaaattga 360
taggtatggt gataggcaac acgccacctc cggttttctc cgctgatttt tcttcatatc 420
ggagcgacag tcgtgcgtta agctggcagc tgacatcgta tgaattaaaa ggaatcttga 480
acaactgccg gccgaagggtg atg ttt tat gac ttg gaa ttt gcc gat ata cta 533
Met Phe Tyr Asp Leu Glu Phe Ala Asp Ile Leu
1 5 10
acg ccg ctc cgc gaa cag ctt cag ttc tgc ctg atg att gaa gcg ggt 581
Thr Pro Leu Arg Glu Gln Leu Gln Phe Cys Leu Met Ile Glu Ala Gly
15 20 25
gcg gga atg aac acg act gaa cag ttt gag agc tta ttt aaa aac agg 629
Ala Gly Met Asn Thr Thr Glu Gln Phe Glu Ser Leu Phe Lys Asn Arg
30 35 40
ccg ctg aag gtg gaa gct gag cag gtg aca gag cat gat ttg gct tta 677
Pro Leu Lys Val Glu Ala Glu Gln Val Thr Glu His Asp Leu Ala Leu
45 50 55
atg ctg ttc acc tcg ggc acg acg gga aac ccg aaa ggc tgc atg gtc 725
Met Leu Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Cys Met Val
60 65 70 75
aac cac ggc agt ctg gcc gca tac ttg aca gag gtg aac gtg aaa tcg 773
Asn His Gly Ser Leu Ala Ala Tyr Leu Thr Glu Val Asn Val Lys Ser
80 85 90
aag cag ctg aaa ggc acg cgc ttt tta gcg agc cac ccg ctc tat cat 821
Lys Gln Leu Lys Gly Thr Arg Phe Leu Ala Ser His Pro Leu Tyr His
95 100 105
atg agc tcg ctc aac cat gtt ttt cag gcg gct ttt gaa gga att gcc 869
Met Ser Ser Leu Asn His Val Phe Gln Ala Ala Phe Glu Gly Ile Ala
110 115 120
ctt tat ttc tta tgg gat ccc gaa ccg ttt gaa atc ctg cag gag atc 917
Leu Tyr Phe Leu Trp Asp Pro Glu Pro Phe Glu Ile Leu Gln Glu Ile
125 130 135
gag aag aaa cgc att cat atg atg atg gcg ttt cct tcc gtc tac acc 965
Glu Lys Lys Arg Ile His Met Met Met Ala Phe Pro Ser Val Tyr Thr
140 145 150 155
tac atg ctg gag gaa atg aaa aga cat cca ttc gac ctg tca tct gtg 1013
Tyr Met Leu Glu Glu Met Lys Arg His Pro Phe Asp Leu Ser Ser Val
160 165 170
aaa atg ctt gtt tcc ggc ggc acc aag gtg ccg gcg cgg ctg att aag 1061
Lys Met Leu Val Ser Gly Gly Thr Lys Val Pro Ala Arg Leu Ile Lys
175 180 185
gag tac aat gac cat gga atc atg atg gtg cag ggg tac ggc agc aca 1109
Glu Tyr Asn Asp His Gly Ile Met Met Val Gln Gly Tyr Gly Ser Thr
190 195 200
gaa gca tgg acg gtc agc gta tgg cgg cct gac atg ggc tgg gat aaa 1157
Glu Ala Trp Thr Val Ser Val Trp Arg Pro Asp Met Gly Trp Asp Lys
205 210 215
gtc act tca gcc ggc aag ccg att ccg caa gtc agc ata aaa atc gaa 1205

10294.000.ST25.txt

Val	Thr	Ser	Ala	Gly	Lys	Pro	Ile	Pro	Gln	Val	Ser	Ile	Lys	Ile	Glu		
220					225					230					235		
gac	cct	gat	aca	cat	gaa	gag	ctg	ccg	acg	gga	gaa	gtc	gga	gaa	gtc		1253
Asp	Pro	Asp	Thr	His	Glu	Glu	Leu	Pro	Thr	Gly	Glu	Val	Gly	Glu	Val		
				240					245					250			
gtc	gtc	aaa	agc	ccg	tat	gtt	ttt	gaa	ggg	tat	tac	caa	aat	cct	tcc		1301
Val	Val	Lys	Ser	Pro	Tyr	Val	Phe	Glu	Gly	Tyr	Tyr	Gln	Asn	Pro	Ser		
			255					260					265				
gcc	acg	caa	aag	gtg	ctg	aaa	gac	ggc	tgg	ttc	tat	atg	ggg	gac	tcc		1349
Ala	Thr	Gln	Lys	Val	Leu	Lys	Asp	Gly	Trp	Phe	Tyr	Met	Gly	Asp	Ser		
		270					275					280					
ggc	aaa	ctc	gat	gaa	gac	gga	ttt	tta	tat	att	acc	ggc	cgg	tat	aaa		1397
Gly	Lys	Leu	Asp	Glu	Asp	Gly	Phe	Leu	Tyr	Ile	Thr	Gly	Arg	Tyr	Lys		
	285					290					295						
gac	gtc	att	gtc	tac	gga	ggc	gac	aac	att	tat	ccg	gac	caa	gtg	gaa		1445
Asp	Val	Ile	Val	Tyr	Gly	Gly	Asp	Asn	Ile	Tyr	Pro	Asp	Gln	Val	Glu		
					305					310					315		
gaa	atc	atc	gat	caa	gtg	ccc	gga	gta	gtt	gaa	tct	gcc	gtc	atc	ggc		1493
Glu	Ile	Ile	Asp	Gln	Val	Pro	Gly	Val	Val	Glu	Ser	Ala	Val	Ile	Gly		
				320					325					330			
gtc	ccg	gat	gaa	atg	tac	ggc	gag	gtt	ccg	agg	gcg	tat	gtg	gtg	aaa		1541
Val	Pro	Asp	Glu	Met	Tyr	Gly	Glu	Val	Pro	Arg	Ala	Tyr	Val	Val	Lys		
			335					340					345				
aat	gaa	agc	gcc	ggc	ctc	aag	aag	gag	gac	att	atc	gcg	tat	tgc	aaa		1589
Asn	Glu	Ser	Ala	Gly	Leu	Lys	Lys	Glu	Asp	Ile	Ile	Ala	Tyr	Cys	Lys		
		350					355					360					
gag	cgc	ctg	tcc	gac	tat	aaa	att	cct	gaa	atc	gtc	ttt	atc	gac	agc		1637
Glu	Arg	Leu	Ser	Asp	Tyr	Lys	Ile	Pro	Glu	Ile	Val	Phe	Ile	Asp	Ser		
	365					370					375						
ctt	ccg	aaa	aac	agg	ctc	ggc	aaa	atc	gtc	aaa	aaa	gat	ctg	cgt	gaa		1685
Leu	Pro	Lys	Asn	Arg	Leu	Gly	Lys	Ile	Val	Lys	Lys	Asp	Leu	Arg	Glu		
					385				390						395		
ctg	gca	gtc	aaa	ggg	cag	tgagc	gcaat	gattg	accga	aagct	tatcc						1733
Leu	Ala	Val	Lys	Gly	Gln												
				400													
agcattggat	aagctttttt	tgctgattcc	ttgcatcagc	tgccgttttt	tgtaacgttt												1793
tccagtgtcta	aaccctactac	aacattagga	ggtgttgaca	attgaaatcg	aaatggagt												1853
caatggtggt	tattgcccgt	cttttattgc	tggccggatg	cgggtgcactg	aaggaggctg												1913
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tcctctcgcc	ttacagtatt	cagcaggcac	ttttgatgac	ggcaaacggt	gccgcgggag												2093
acagcagaaa	ggacctgatc	agcactttac	atctcagcca	ggcggatatg	gcacatgatca												2153
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<210> 68

<211> 401

<212> PRT

<213> Bacillus licheniformis

<400> 68

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 20 25 30
 Thr Glu Gln Phe Glu Ser Leu Phe Lys Asn Arg Pro Leu Lys Val Glu
 35 40 45
 Ala Glu Gln Val Thr Glu His Asp Leu Ala Leu Met Leu Phe Thr Ser
 50 55 60
 Gly Thr Thr Gly Asn Pro Lys Gly Cys Met Val Asn His Gly Ser Leu
 65 70 75 80
 Ala Ala Tyr Leu Thr Glu Val Asn Val Lys Ser Lys Gln Leu Lys Gly
 85 90 95
 Thr Arg Phe Leu Ala Ser His Pro Leu Tyr His Met Ser Ser Leu Asn
 100 105 110
 His Val Phe Gln Ala Ala Phe Glu Gly Ile Ala Leu Tyr Phe Leu Trp
 115 120 125
 Asp Pro Glu Pro Phe Glu Ile Leu Gln Glu Ile Glu Lys Lys Arg Ile
 130 135 140
 His Met Met Met Ala Phe Pro Ser Val Tyr Thr Tyr Met Leu Glu Glu
 145 150 155 160
 Met Lys Arg His Pro Phe Asp Leu Ser Ser Val Lys Met Leu Val Ser
 165 170 175
 Gly Gly Thr Lys Val Pro Ala Arg Leu Ile Lys Glu Tyr Asn Asp His
 180 185 190
 Gly Ile Met Met Val Gln Gly Tyr Gly Ser Thr Glu Ala Trp Thr Val
 195 200 205
 Ser Val Trp Arg Pro Asp Met Gly Trp Asp Lys Val Thr Ser Ala Gly
 210 215 220
 Lys Pro Ile Pro Gln Val Ser Ile Lys Ile Glu Asp Pro Asp Thr His
 225 230 235 240

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Glu Glu Leu Pro Thr Gly Glu Val Gly Glu Val Val Val Lys Ser Pro
245 250 255

Tyr Val Phe Glu Gly Tyr Tyr Gln Asn Pro Ser Ala Thr Gln Lys Val
260 265 270

Leu Lys Asp Gly Trp Phe Tyr Met Gly Asp Ser Gly Lys Leu Asp Glu
275 280 285

Asp₂₉₀ Gly Phe Leu Tyr Ile Thr₂₉₅ Gly Arg Tyr Lys Asp₃₀₀ Val Ile Val Tyr

Gly Gly Asp Asn Ile Tyr Pro Asp Gln Val Glu Glu Ile Ile Asp Gln
305 310 315 320

Val Pro Gly Val Val Glu Ser Ala Val Ile Gly Val Pro Asp Glu Met
325 330 335

Tyr Gly Glu Val Pro Arg Ala Tyr Val Val Lys Asn Glu Ser Ala Gly
340 345 350

Leu Lys Lys Glu Asp Ile Ile Ala Tyr Cys Lys Glu Arg Leu Ser Asp
355 360 365

Tyr Lys Ile Pro Glu Ile Val Phe Ile Asp Ser Leu Pro Lys Asn Arg
370 375 380

Leu Gly Lys Ile Val Lys Lys Asp Leu Arg Glu Leu Ala Val Lys Gly
385 390 395 400

Gln

<210> 69

<211> 1547

<212> DNA

<213> **Bacillus licheniformis**

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<221> CDS

<222> (501)..(1046)

<223>

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10294.000.ST25.txt

tggctccgcc tgatcgtttc atcccctgta tatccataga tttcagcggc ttcaaccatc 180
 atttgccgct tcttgctgat ggaaacgagc aatgcttctt tttcaatata cctttgcacc 240
 cgctccccggg aggtcccaaa aaaatttttt tgcaaaaaaa aatttttccc cataaggctc 300
 tagtgttatg agaaaaaat ccgggaacgg aatcaaggac cataaaaatt ttttctggcc 360
 aacccaaaac cccggtgctg ttaagtcgtc ataaataaga aaccagcggg ggaataattt 420
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 tatttaagga gagaggacca ttg aaa aag tta atc gtt tgt tta tta gct gtt 533
 Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val
 1 5 10
 tta ctg atc ttg cct gcc gga gcg tcc ctc gca gcg aaa aat caa aca 581
 Leu Leu Ile Leu Pro Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr
 15 20 25
 tca ggg aat tta aca aat aag caa gtc atg caa tta acc ttg cag gca 629
 Ser Gly Asn Leu Thr Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala
 30 35 40
 cgg gag cac ttt tgg aat acg atg agc ggc cac aat cca aaa gcg aaa 677
 Arg Glu His Phe Trp Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys
 45 50 55
 aac tca act tgc cca tcc aaa aca ttt gaa tac cgc ggt ctt cca tat 725
 Asn Ser Thr Cys Pro Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr
 60 65 70 75
 acg tat atg tgc agt gaa ttc agc aca aaa gca aaa tta aca gac tac 773
 Thr Tyr Met Cys Ser Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr
 80 85 90
 ttg acg ccg gtt ttc aca aaa gac gcc att aaa aaa ggc ttg gaa aaa 821
 Leu Thr Pro Val Phe Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys
 95 100 105
 tac aac atc att tct tat aaa gga aaa atg gcc gtg cct gtc ggc gat 869
 Tyr Asn Ile Ile Ser Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp
 110 115 120
 ggg gac aac ctc tta gga tgg gac aag gca aaa atc aaa ctg atc tct 917
 Gly Asp Asn Leu Leu Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser
 125 130 135
 caa aaa aac aat acc cgc act tat gaa ttt tcc gta ccg gca ttg gat 965
 Gln Lys Asn Asn Thr Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp
 140 145 150 155
 gga tcg gtg act gcg aaa aga aag atc acg ttt gtg aaa gaa aac aac 1013
 Gly Ser Val Thr Ala Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn
 160 165 170
 aaa tgg aaa atc aat cag ctc gat gct gcc atc taaacgaaaa agctaattgtc 1066
 Lys Trp Lys Ile Asn Gln Leu Asp Ala Ala Ile
 175 180
 taaaaacgga cattagcttt tttccgtcaa acggtcagtt caacgatgtt gccgtcagga 1126
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10294.000.ST25.txt

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 tcctctaaat tgttcgtcca tatggcgatg tgttcgattt tcataaatct ccctccatt 1486
 tcatattacc atatagatcc tctgcctttt tttacacttt tttaaattga taagtattca 1546
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<210> 70

<211> 182

<212> PRT

<213> Bacillus licheniformis

<400> 70

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 20 25 30

Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala Arg Glu His Phe Trp
 35 40 45

Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys Asn Ser Thr Cys Pro
 50 55 60

Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr Thr Tyr Met Cys Ser
 65 70 75 80

Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr Leu Thr Pro Val Phe
 85 90 95

Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys Tyr Asn Ile Ile Ser
 100 105 110

Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp Gly Asp Asn Leu Leu
 115 120 125

Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser Gln Lys Asn Asn Thr
 130 135 140

Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp Gly Ser Val Thr Ala
 145 150 155 160

Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn Lys Trp Lys Ile Asn
 165 170 175

10294.000.ST25.txt

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ata tcg gcg ctt aac aat cga ttt ccg gaa tgg atc ttt aag aaa atg Ile Ser Ala Leu Asn Asn Arg Phe Pro Glu Trp Ile Phe Lys Lys Met 155 160 165	774
cta tcc tcc ttt act aca ctt cct gct gat cag gcg atg ctg aaa gtc Leu Ser Ser Phe Thr Thr Leu Pro Ala Asp Gln Ala Met Leu Lys Val 170 175 180	822
acg gag gga gat att gaa gaa atg aga aaa atg aac aac aga cag cgt Thr Glu Gly Asp Ile Glu Glu Met Arg Lys Met Asn Asn Arg Gln Arg 185 190 195 200	870
tca agt cga ggg ttc ttg ctt gat tta aaa aat ata gac gat tta tct Ser Ser Arg Gly Phe Leu Leu Asp Leu Lys Asn Ile Asp Asp Leu Ser 205 210 215	918
ttc cat cat ttg aag gag att tct tgt ccg gta tta att atg cat tgc Phe His His Leu Lys Glu Ile Ser Cys Pro Val Leu Ile Met His Cys 220 225 230	966
cga tat gat cgt gtt gtt cca gcc gag cat gct ttt cat gca aaa aaa Arg Tyr Asp Arg Val Val Pro Ala Glu His Ala Phe His Ala Lys Lys 235 240 245	1014
ctg att cct ttt tca gaa gtc tat cag gca gac agc tgg ggt cat ctc Leu Ile Pro Phe Ser Glu Val Tyr Gln Ala Asp Ser Trp Gly His Leu 250 255 260	1062
att tgg ctg gga aca gag ggt aaa tct gtc tca cag aag gtc atc agc Ile Trp Leu Gly Thr Glu Gly Lys Ser Val Ser Gln Lys Val Ile Ser 265 270 275 280	1110
ttt tta aaa acc acatcatctt gatcataaga tgaataaaaat tttaggatcg Phe Leu Lys Thr	1162
cagcctaccc gcaaatgaag tagtgcaatt ttttaatcaa gagcagaatg atctttccga	1222
acagaactga tgaacgtcgt acaagacttg caaataagat gaatgagaaa tcctccctgg	1282
ccggttttcg gagcacaagg gaaacttatg tataagaatc tattccgata gagggacagg	1342
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ggcaagcggc agcttcttcc taaactcgcg attgaaacga tgcggctatg caatatggtg	1582
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<212> PRT	
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<400> 72

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 20 25 30

Ser Phe Glu Leu Pro Arg Gly Ile Trp Val Ser Arg Ser Leu Leu Glu
 35 40 45

Pro Ile Leu Tyr His His Ala Phe Pro Cys Arg Val Trp Pro Asp Ile
 50 55 60

Glu Arg Asn Arg Gly Gln Phe Gly Thr Cys Leu Leu Leu His Met Lys
 65 70 75 80

Leu Leu Asp His Leu Asn Ile Lys Lys Val His Val Val Ala Val Ser
 85 90 95

Ala Gly Gly Pro Ser Gly Ile Cys Phe Ala Ser Lys Tyr Ser Glu Arg
 100 105 110

Val Glu Ser Leu Ile Leu Gln Ser Ala Val Thr Lys Gln Trp Leu Thr
 115 120 125

Ala Lys Asp Ile Glu Tyr Lys Val Gly Gln Ile Ile Phe Arg Pro Pro
 130 135 140

Val Glu Lys Ala Val Trp Lys Leu Ile Ser Ala Leu Asn Asn Arg Phe
 145 150 155 160

Pro Glu Trp Ile Phe Lys Lys Met Leu Ser Ser Phe Thr Thr Leu Pro
 165 170 175

Ala Asp Gln Ala Met Leu Lys Val Thr Glu Gly Asp Ile Glu Glu Met
 180 185 190

Arg Lys Met Asn Asn Arg Gln Arg Ser Ser Arg Gly Phe Leu Leu Asp
 195 200 205

Leu Lys Asn Ile Asp Asp Leu Ser Phe His His Leu Lys Glu Ile Ser
 210 215 220

Cys Pro Val Leu Ile Met His Cys Arg Tyr Asp Arg Val Val Pro Ala
 225 230 235 240

Glu His Ala Phe His Ala Lys Lys Leu Ile Pro Phe Ser Glu Val Tyr
 245 250 255

Gln Ala Asp Ser Trp Gly His Leu Ile Trp Leu Gly Thr Glu Gly Lys
 260 265 270

10294.000.ST25.txt

Ser Val Ser Gln Lys Val Ile Ser Phe Leu Lys Thr
275 280

<210> 73

<211> 1630

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (256)..(1131)

<223>

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 tttttggcca ttatatgaat tcggccagcg ttgaatatatt cctcttttca gggaaatttc 180
 cgaagcggcg attcaaaaat ccgcaaactt atcttacaat agaaaaagtt ctgaatgac 240
 gagtagggag agatc gtt agt atg aaa gta tgc gtt ctg ttt gtc ttg ctt 291
 Val Ser Met Lys Val Ser Val Leu Phe Val Leu Leu
 1 5 10
 gcg gca att tta tgg gga acg acg gga aca acc cag gca ttt gcg ccg 339
 Ala Ala Ile Leu Trp Gly Thr Thr Gly Thr Thr Gln Ala Phe Ala Pro
 15 20 25
 aaa gag gcg gca cct ctt gtg ttc ggc gct gtc aga atg gct gtc ggc 387
 Lys Glu Ala Ala Pro Leu Val Phe Gly Ala Val Arg Met Ala Val Gly
 30 35 40
 ggc atc acc ctg ctc ttg ttc gcg gct ttc cgc ggt caa ttg aaa cga 435
 Gly Ile Thr Leu Leu Leu Phe Ala Ala Phe Arg Gly Gln Leu Lys Arg
 45 50 55 60
 agc ggc tgg ccc gtt aaa acg ctg atc atc gca gca ttg agc atg gca 483
 Ser Gly Trp Pro Val Lys Thr Leu Ile Ile Ala Ala Leu Ser Met Ala
 65 70 75
 ttt tac cag cct ttc ttt ttt tca gcc gtc agc ctg tca gga atc gcc 531
 Phe Tyr Gln Pro Phe Phe Phe Ser Ala Val Ser Leu Ser Gly Ile Ala
 80 85 90
 gtc gga acg gtc gtc gcc atc ggc agc gct ccg att att gcc ggc tgc 579
 Val Gly Thr Val Val Ala Ile Gly Ser Ala Pro Ile Ile Ala Gly Cys
 95 100 105
 ctc gaa tgg ctg gtg ttc aaa aag gtt ccg cag acg aaa tgg tgg atc 627
 Leu Glu Trp Leu Val Phe Lys Lys Val Pro Gln Thr Lys Trp Trp Ile
 110 115 120
 gca act gct gca gcg ata gca ggc gta gcc tta tta ttc att ccc tcc 675

10294.000.ST25.txt

Ala Thr Ala Ala Ala Ile Ala Gly Val Ala Leu Leu Phe Ile Pro Ser
125 130 135 140

gcc tca tcg ggg ggg agc ttt ctc ggc ata ctg ctc gca ctt ggc gcc 723
Ala Ser Ser Gly Gly Ser Phe Leu Gly Ile Leu Leu Ala Leu Gly Ala 155

ggt ctt tcc ttt gcc gtc tac acg ctg aca agc aag aaa ctc ctg caa 771
Gly Leu Ser Phe Ala Val Tyr Thr Leu Thr Ser Lys Lys Leu Leu Gln 160 170

aag caa aag ccg gag gct gtc aca ggc acc gta ttc ttt tta agc gct 819
Lys Gln Lys Pro Glu Ala Val Thr Gly Thr Val Phe Phe Leu Ser Ala 175 185

gta ttg ctt gcc ccg ttg ttg ttt ctg tac gat ctc ggc tgg atc tca 867
Val Leu Leu Ala Pro Leu Leu Phe Leu Tyr Asp Leu Gly Trp Ile Ser 190 200

tcg gtt cag gga atg gct gtc agc ctc tat atc ggg gtc att gca acc 915
Ser Val Gln Gly Met Ala Val Ser Leu Tyr Ile Gly Val Ile Ala Thr 205 210 215 220

gga gcc gcg tac ctg tta ttt acg aca gga ttg gca aaa gtg ccc gcc 963
Gly Ala Ala Tyr Leu Leu Phe Thr Thr Gly Leu Ala Lys Val Pro Ala 225 230 235

tca acg gcg gtg acg ctg tcg ctt gct gaa ccg ctt aca gcg tcg ctg 1011
Ser Thr Ala Val Thr Leu Ser Leu Ala Glu Pro Leu Thr Ala Ser Leu 240 245 250

ttg gga acc gtg ctt gtc agg gaa tcg ctg cct ctt gtt tcc tgg gcc 1059
Leu Gly Thr Val Leu Val Arg Glu Ser Leu Pro Leu Val Ser Trp Ala 255 260 265

ggg atc gcc ctg ctt ctt tta ggc att ttt tat att tcc tat cag ccc 1107
Gly Ile Ala Leu Leu Leu Leu Gly Ile Phe Tyr Ile Ser Tyr Gln Pro 270 275 280

aaa aag gat aaa ata aac gct gaa cagatgaaag cgtaaaaaaa acccgcccgg 1161
Lys Lys Asp Lys Ile Asn Ala Glu 285 290

ggatatacgg gcggggttttc atgttgctctt gttattcatc caaaccgatg gacaaatatt 1221

ttgtttccaa atacggctcg atgccttcca gtccgctttc gcgtccgata ccgctttcct 1281

tcatgccgcc gaaaggcgcc tgaacgggtg acgggtccgcc gtcattccag ccgagaatgc 1341

cgtaatcaag gtttttcggat aaatagatgc cgcggcggtg gttttccgta aagaagtatg 1401

ccgctaaacc gtaaggcgta tcattggcga gcttgaccgc ttcgtccagc gttttaaaag 1461

acgtaatcgg cgcaacgggg ccgaatgttt cctcatgcat gatcgtcatt gaaggatcaa 1521

catccgtcag cactgtcgga tggacaaagt agcatgattt ctcatcatcg ctttcatatt 1581

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<211> 292

<212> PRT

<213> Bacillus licheniformis

<400> 74

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 20 25 30

Pro Leu Val Phe Gly Ala Val Arg Met Ala Val Gly Gly Ile Thr Leu
 35 40 45

Leu Leu Phe Ala Ala Phe Arg Gly Gln Leu Lys Arg Ser Gly Trp Pro
 50 55 60

Val Lys Thr Leu Ile Ile Ala Ala Leu Ser Met Ala Phe Tyr Gln Pro
 65 70 75 80

Phe Phe Phe Ser Ala Val Ser Leu Ser Gly Ile Ala Val Gly Thr Val
 85 90 95

Val Ala Ile Gly Ser Ala Pro Ile Ile Ala Gly Cys Leu Glu Trp Leu
 100 105 110

Val Phe Lys Lys Val Pro Gln Thr Lys Trp Trp Ile Ala Thr Ala Ala
 115 120 125

Ala Ile Ala Gly Val Ala Leu Leu Phe Ile Pro Ser Ala Ser Ser Gly
 130 135 140

Gly Ser Phe Leu Gly Ile Leu Leu Ala Leu Gly Ala Gly Leu Ser Phe
 145 150 155 160

Ala Val Tyr Thr Leu Thr Ser Lys Lys Leu Leu Gln Lys Gln Lys Pro
 165 170 175

Glu Ala Val Thr Gly Thr Val Phe Phe Leu Ser Ala Val Leu Leu Ala
 180 185 190

Pro Leu Leu Phe Leu Tyr Asp Leu Gly Trp Ile Ser Ser Val Gln Gly
 195 200 205

Met Ala Val Ser Leu Tyr Ile Gly Val Ile Ala Thr Gly Ala Ala Tyr
 210 215 220

Leu Leu Phe Thr Thr Gly Leu Ala Lys Val Pro Ala Ser Thr Ala Val
 225 230 235 240

Thr Leu Ser Leu Ala Glu Pro Leu Thr Ala Ser Leu Leu Gly Thr Val
 245 250 255

10294.000.ST25.txt

Leu Val Arg Glu Ser Leu Pro Leu Val Ser Trp Ala Gly Ile Ala Leu
 260 265 270

Leu Leu Leu Gly Ile Phe Tyr Ile Ser Tyr Gln Pro Lys Lys Asp Lys
 275 280 285

Ile Asn Ala Glu
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<210> 75
 <211> 2140
 <212> DNA
 <213> Bacillus licheniformis

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 <222> (501)..(1637)
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ttacagtaat gcctacactg atatggactg tgaggcgatg actgaagata ttaatcattt	180
gaaatctgcc aatcctgagg tgtatcaaaa gctgcagaag atggacatta ccgctgcggc	240
gggatacaga acagaggata ctgtaagttt ttccccttac tataaccgcaa gcggaaaaca	300
taaaataaac agtgatgata tcgtttcggg cgaaagtcaa cacggtgaca tattaggcga	360
tctcattgat aaaaagccag aaattgaagt aagaggttcc ggtgtaacca atcctggaca	420
tatttatgaa attgaagact ctgaatttgt tgacttgatt cgagagggtca acaaaaaaga	480
agcagaatag gagaagggtcg atg aaa aag aaa ggg ttt ata agt ata ttt ttt	533
Met Lys Lys Lys Gly Phe Ile Ser Ile Phe Phe	10
1 5	
tta ata gtg ttt cta ctg ctc gcc acc acc ggc tgc ggc aaa gat gat	581
Leu Ile Val Phe Leu Leu Leu Ala Thr Thr Gly Cys Gly Lys Asp Asp	25
15 20	
gtt cag gaa gcc atc tat aaa aaa ggc ttg ccc aaa gaa gac agt cca	629
Val Gln Glu Ala Ile Tyr Lys Lys Gly Leu Pro Lys Glu Asp Ser Pro	40
30 35	
gca ttt aga gaa ttt atg aga cat gaa ctt gat tta gcg aca gac gca	677
Ala Phe Arg Glu Phe Met Arg His Glu Leu Asp Leu Ala Thr Asp Ala	55
45 50	
act ctt agt tat caa aat agt aca tat acg att atg cgc agt gat aaa	725
Thr Leu Ser Tyr Gln Asn Ser Thr Tyr Thr Ile Met Arg Ser Asp Lys	70 75
60 65	

10294.000.ST25.txt

aag ggg cta cgg tac tat caa tat aca gat caa gaa gta gac gat ttt 773
Lys Gly Leu Arg Tyr Tyr Gln Tyr Thr Asp Gln Glu Val Asp Asp Phe
80 85 90

tac agt ccc ttt ctt tcg gct aat aaa tat cct gcg aca aaa tta tat 821
Tyr Ser Pro Phe Leu Ser Ala Asn Lys Tyr Pro Ala Thr Lys Leu Tyr
95 100 105

gat ttg aaa aca act gaa ttt tta act aaa gaa aaa ctt atc cac aat 869
Asp Leu Lys Thr Thr Glu Phe Leu Thr Lys Glu Lys Leu Ile His Asn
110 115 120

aaa ctt gaa tat aat ctg ccg gaa atg aca tta gat aaa aag aat gtt 917
Lys Leu Glu Tyr Asn Leu Pro Glu Met Thr Leu Asp Lys Lys Asn Val
125 130 135

cta aaa gtg aaa aca aaa agc gga gaa aaa aaa ata gag ttt cca tca 965
Leu Lys Val Lys Thr Lys Ser Gly Glu Lys Lys Ile Glu Phe Pro Ser
140 145 150 155

gcc aag gat aaa aaa gta cat ctg gcg tta gca gct gtt agc aaa gac 1013
Ala Lys Asp Lys Lys Val His Leu Ala Leu Ala Val Ser Lys Asp
160 165 170

agc atg ctt ata caa gtg gac gta tat gaa aaa ttt aaa aat ggt gac 1061
Ser Met Leu Ile Gln Val Asp Val Tyr Glu Lys Phe Lys Asn Gly Asp
175 180 185

ctt gga gac aga caa ata tat tat ctt ttt tta aaa agt gat ctt tca 1109
Leu Gly Asp Arg Gln Ile Tyr Tyr Leu Phe Leu Lys Ser Asp Leu Ser
190 195 200

aaa tac cgg att gtt aaa gaa gag gaa tta aat tca aca att gag tct 1157
Lys Tyr Arg Ile Val Lys Glu Glu Leu Asn Ser Thr Ile Glu Ser
205 210 215

ggg aaa ctg aag gaa tac tta tcc gta ttt cca aat gta gcg aag gat 1205
Gly Lys Leu Lys Glu Tyr Leu Ser Val Phe Pro Asn Val Ala Lys Asp
220 225 230 235

gga gca tat cgt aag tta ttt gat aaa tac att ttt gat gaa aag aaa 1253
Gly Ala Tyr Arg Lys Leu Phe Asp Lys Tyr Ile Phe Asp Glu Lys Lys
240 245 250

aac aaa gtt agg aaa atc aaa aac act gat att ctg agc aaa gac ggt 1301
Asn Lys Val Arg Lys Ile Lys Asn Thr Asp Ile Leu Ser Lys Asp Gly
255 260 265

aag tat gtt tat att aac gga gca aaa gaa aaa gaa aca aat gta atg 1349
Lys Tyr Val Tyr Ile Asn Gly Ala Lys Glu Lys Glu Thr Asn Val Met
270 275 280

cct gat ggt atc caa cag ata caa aca atg gat aat tat cta aaa gga 1397
Pro Asp Gly Ile Gln Gln Ile Gln Thr Met Asp Asn Tyr Leu Lys Gly
285 290 295

aat gaa aaa tat gaa gct caa ttt aag att gat ttc aaa caa att gca 1445
Asn Glu Lys Tyr Glu Ala Gln Phe Lys Ile Asp Phe Lys Gln Ile Ala
300 305 310 315

aaa gag atg gat tta aac gcg ggt gat gcg agg ata gct aat att cat 1493
Lys Glu Met Asp Leu Asn Ala Gly Asp Ala Arg Ile Ala Asn Ile His
320 325 330

tat ttt aat aaa gat tat gta gtt ttg tat att tct tat cat ggg aag 1541
Tyr Phe Asn Lys Asp Tyr Val Val Leu Tyr Ile Ser Tyr His Gly Lys
335 340 345

10294.000.ST25.txt

aca att ggt aca gca ggt tct gtt aat gta ctt att gat tta caa aaa 1589
 Thr Ile Gly Thr Ala Gly Ser Val Asn Val Leu Ile Asp Leu Gln Lys
 350 355 360

aac aaa caa cag cca acg gct tat tta gtt gat tta gga att gaa tca 1637
 Asn Lys Gln Gln Pro Thr Ala Tyr Leu Val Asp Leu Gly Ile Glu Ser
 365 370 375

tagagggact gaagagtttt tatgcagtcc ttttcttatt tgacaaagggt aggccacaaa 1697
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<210> 76

<211> 379

<212> PRT

<213> Bacillus licheniformis

<400> 76

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 20 25 30

Tyr Lys Lys Gly Leu Pro Lys Glu Asp Ser Pro Ala Phe Arg Glu Phe
 35 40 45

Met Arg His Glu Leu Asp Leu Ala Thr Asp Ala Thr Leu Ser Tyr Gln
 50 55 60

Asn Ser Thr Tyr Thr Ile Met Arg Ser Asp Lys Lys Gly Leu Arg Tyr
 65 70 75 80

Tyr Gln Tyr Thr Asp Gln Glu Val Asp Asp Phe Tyr Ser Pro Phe Leu
 85 90 95

Ser Ala Asn Lys Tyr Pro Ala Thr Lys Leu Tyr Asp Leu Lys Thr Thr
 100 105 110

Glu Phe Leu Thr Lys Glu Lys Leu Ile His Asn Lys Leu Glu Tyr Asn
 115 120 125

Leu Pro Glu Met Thr Leu Asp Lys Lys Asn Val Leu Lys Val Lys Thr
 130 135 140

Lys Ser Gly Glu Lys Lys Ile Glu Phe Pro Ser Ala Lys Asp Lys Lys
 145 150 155 160

Val His Leu Ala Leu Ala Ala Val Ser Lys Asp Ser Met Leu Ile Gln
 165 170 175

Val Asp Val Tyr Glu Lys Phe Lys Asn Gly Asp Leu Gly Asp Arg Gln
 180 185 190

Ile Tyr Tyr Leu Phe Leu Lys Ser Asp Leu Ser Lys Tyr Arg Ile Val
 195 200 205

Lys Glu Glu Glu Leu Asn Ser Thr Ile Glu Ser Gly Lys Leu Lys Glu
 210 215 220

Tyr Leu Ser Val Phe Pro Asn Val Ala Lys Asp Gly Ala Tyr Arg Lys
 225 230 235 240

Leu Phe Asp Lys Tyr Ile Phe Asp Glu Lys Lys Asn Lys Val Arg Lys
 245 250 255

Ile Lys Asn Thr Asp Ile Leu Ser Lys Asp Gly Lys Tyr Val Tyr Ile
 260 265 270

Asn Gly Ala Lys Glu Lys Glu Thr Asn Val Met Pro Asp Gly Ile Gln
 275 280 285

Gln Ile Gln Thr Met Asp Asn Tyr Leu Lys Gly Asn Glu Lys Tyr Glu
 290 295 300

Ala Gln Phe Lys Ile Asp Phe Lys Gln Ile Ala Lys Glu Met Asp Leu
 305 310 315 320

Asn Ala Gly Asp Ala Arg Ile Ala Asn Ile His Tyr Phe Asn Lys Asp
 325 330 335

Tyr Val Val Leu Tyr Ile Ser Tyr His Gly Lys Thr Ile Gly Thr Ala
 340 345 350

Gly Ser Val Asn Val Leu Ile Asp Leu Gln Lys Asn Lys Gln Gln Pro
 355 360 365

Thr Ala Tyr Leu Val Asp Leu Gly Ile Glu Ser
 370 375

<210> 77

<211> 1387

<212> DNA

<213> *Bacillus licheniformis*

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<222> (501)..(884)

<223>

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acgcaaattgt agttgatgag ttaaacgtat ttccggttcc ggacggagat acgggaacga    240
acactaatct gtcgatgaca tccggtgcga aagaagtggg gcaaatcgac accgccaata    300
tcggcaaagt ggcacaaagc ctgtcaaggg ggcttctgat gggggcgagg ggaaactcgg    360
gcgtcatttt atcccagctg ttcagaggct ttggcaaatac gattgaacag aaatcggaaa    420
ttaacgcgaa agaatttgcc gccgcgttcc aggccggagt ggacaccgcc tacaaggccg    480
tcataaacia gcttctacag atg tct acc agc agc att gtc gtt ctc ttg att    533
                Met Ser Thr Ser Ser Ile Val Val Leu Leu Ile
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tgc gcc gcg ctc atc atc tac gcg gtc gct tca tac atc tat cag cag      581
cys ala ala leu ile ile tyr ala val ala ser tyr ile tyr gln gln
                15         20         25

cgc att atg aaa acc ttg aca gaa gaa gaa ttc cgg gca ggc tat cgc      629
arg ile met lys thr leu thr glu glu glu phe arg ala gly tyr arg
                30         35         40

aaa gcg cag ctc atc gat gtg cgc gag ccg aat gag tat gaa ggc ggc      677
lys ala gln leu ile asp val arg glu pro asn glu tyr glu gly gly
                45         50         55

cac att ttg ggt gcg aga aac att ccg ctt tca cag ctt aag caa aga      725
his ile leu gly ala arg asn ile pro leu ser gln leu lys gln arg
                60         65         70         75

aaa agc gaa atc cgg cct gac aaa ccg gtt tac ctg tac tgc caa aac      773
lys ser glu ile arg pro asp lys pro val tyr leu tyr cys gln asn
                80         85         90

aac gtc aga agc gga agg gcc gcc caa acg ctc cgc aaa cac ggc tgt      821
asn val arg ser gly arg ala ala gln thr leu arg lys his gly cys
                95         100         105

aag gag att tac aac ctg aaa ggc ggg ttc aaa aaa tgg ggc gga aaa      869
lys glu ile tyr asn leu lys gly gly phe lys lys trp gly gly lys
                110         115         120

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10294.000.ST25.txt

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Ile Lys Thr Lys Asn
125

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cgggtgatga gcggttatcc ctttccggca aaaataagcc ggcgagatgg gttcgccggc 1044
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<210> 78

<211> 128

<212> PRT

<213> Bacillus licheniformis

<400> 78

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Ile Tyr Ala Val Ala Ser Tyr Ile Tyr Gln Gln Arg Ile Met Lys Thr
20 25 30

Leu Thr Glu Glu Glu Phe Arg Ala Gly Tyr Arg Lys Ala Gln Leu Ile
35 40 45

Asp Val Arg Glu Pro Asn Glu Tyr Glu Gly Gly His Ile Leu Gly Ala
50 55 60

Arg Asn Ile Pro Leu Ser Gln Leu Lys Gln Arg Lys Ser Glu Ile Arg
65 70 75 80

Pro Asp Lys Pro Val Tyr Leu Tyr Cys Gln Asn Asn Val Arg Ser Gly
85 90 95

Arg Ala Ala Gln Thr Leu Arg Lys His Gly Cys Lys Glu Ile Tyr Asn
100 105 110

Leu Lys Gly Gly Phe Lys Lys Trp Gly Gly Lys Ile Lys Thr Lys Asn
115 120 125

<210> 79

<211> 1486

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(983)

<223>

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cgt acg gca atg gat cag aaa gaa aac ggc cac gag cag gct gcc gaa Arg Thr Ala Met Asp Gln Lys Glu Asn Gly His Glu Gln Ala Ala Glu <div style="text-align:center;">30 35 40</div>	629
aka gcc agg cag gaa gcc ggc tta aaa caa gtt gac agc gtg gag acg Thr Ala Arg Gln Glu Ala Gly Leu Lys Gln Val Asp Ser Val Glu Thr <div style="text-align:center;">45 50 55</div>	677
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ett tac aaa aaa gca tca gcc ggc att acc ggc cgc cag gct gca aaa Leu Tyr Lys Lys Ala Ser Ala Gly Ile Thr Gly Arg Gln Ala Ala Lys <div style="text-align:center;">95 100 105</div>	821
gct gtt cag gat gag ggc etg atg tct gag ett aaa gag gtg cac ett Ala Val Gln Asp Glu Gly Leu Met Ser Glu Leu Lys Glu Val His Leu <div style="text-align:center;">110 115 120</div>	869
gca agg gaa ggc aat gtt eta ttg tgg gaa gtt aka tac tta aat aaa	917

Page 165

Ala Arg Glu Gly Asn Val Leu Leu Trp Glu Val Thr Tyr Leu Asn Lys
 125 130 135

gat ggg cag tac agt tta agc tat gtg gac ttt ata aac gga aaa att 965
 Asp Gly Gln Tyr Ser Leu Ser Tyr Val Asp Phe Ile Asn Gly Lys Ile
 140 145 150 155

cac aaa aat att acg cct tagacgaaac aggggggaaat cgagttgaat 1013
 His Lys Asn Ile Thr Pro
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Gln Lys Glu Asn Gly His Glu Gln Ala Ala Glu Thr Ala Arg Gln Glu
 35 40 45

Ala Gly Leu Lys Gln Val Asp Ser Val Glu Thr Phe Val Gly Lys Glu
 50 55 60

Lys Gln Tyr Ile Val Thr Gly Ala Asp Lys Lys Gly Asp Lys Met Tyr
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Val Trp Val Pro Ala Asp Lys Lys Gln Lys Thr Leu Tyr Lys Lys Ala
 85 90 95

Ser Ala Gly Ile Thr Gly Arg Gln Ala Ala Lys Ala Val Gln Asp Glu
 100 105 110

Gly Leu Met Ser Glu Leu Lys Glu Val His Leu Ala Arg Glu Gly Asn
 115 120 125

Val Leu Leu Trp Glu Val Thr Tyr Leu Asn Lys Asp Gly Gln Tyr Ser
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 atc gca gcc gga atc atc cta cta gct gtc ttc ttt aca ttc gtc ccg 581
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 30 35 40
 ttc aca ctg atc gga atg agg ctc cgc cgc gtc att cca aac cgc gtg 677
 Phe Thr Leu Ile Gly Met Arg Leu Arg Arg Val Ile Pro Asn Arg Val
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aat Asn	cag Gln	ctg Leu	gaa Glu	agc Ser 80	cac His	tat Tyr	ctt Leu	gca Ala	ggg Gly 85	ggt Gly	aat Asn	gtt Val	gac Asp	cgg Arg 90	gtc Val	773
gtc Val	aac Asn	gcg Ala	ctt Leu 95	atc Ile	gct Ala	gcc Ala	caa Gln	cgt Arg 100	gca Ala	aac Asn	att Ile	gaa Glu 105	ctt Leu	aca Thr	ttc Phe	821
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cgc Arg	gtc Val	gaa Glu 270	gaa Glu	atg Met	cgc Arg	gcc Ala	aaa Lys 275	gtc Val	gtc Val	gaa Glu	gcc Ala	gaa Glu	gcc Ala	gaa Glu	gtg Val	1349
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gac Asp 300	tac Tyr	ctc Leu	aat Asn	atg Met	aaa Lys 305	aac Asn	atc Ile	gac Asp	gcc Ala	gac Asp 310	act Thr	gac Asp	atg Met	cgc Arg	gat Asp 315	1445
tct Ser	ttc Phe	gga Gly	aag Lys	atg Met 320	acg Thr	aaa Lys	gac Asp	caa Gln	aat Asn 325	gaa Glu	gag Glu	gat Asp	cat His	aaa Lys 330		1490

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<213> Bacillus licheniformis

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 35 40 45

Met Arg Leu Arg Arg Val Ile Pro Asn Arg Val Val Asn Pro Leu Ile
 50 55 60

Lys Ala His Lys Ala Gly Leu Asp Val Ala Ile Asn Gln Leu Glu Ser
 65 70 75 80

His Tyr Leu Ala Gly Gly Asn Val Asp Arg Val Val Asn Ala Leu Ile
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Ala Ala Gln Arg Ala Asn Ile Glu Leu Thr Phe Ala Arg Cys Ala Ala
 100 105 110

Ile Asp Leu Ala Gly Arg Asp Val Leu Glu Ala Val Gln Met Ser Val
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Asp Arg Leu Val Gly Gly Ala Gly Glu Glu Thr Ile Ile Ala Arg Val
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Val Leu Glu Asn Pro Asp Met Ile Ser Gln Thr Val Leu Ser Lys Gly
 195 200 205

Leu Asp Ser Gly Thr Ala Phe Glu Ile Leu Ser Ile Asp Ile Ala Asp
 210 215 220

Val Asp Ile Gly Lys Asn Ile Gly Ala Ile Leu Gln Thr Asp Gln Ala
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Glu Ala Asp Lys Asn Ile Ala Gln Ala Lys Ala Glu Glu Arg Arg Ala
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Arg Ala Lys Val Val Glu Ala Glu Ala Glu Val Pro Leu Ala Met Ser
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Glu Ala Leu Arg Ser Gly Lys Ile Gly Val Met Asp Tyr Leu Asn Met
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 Thr Gly Tyr Gln Asn Leu Lys Tyr Leu Gly Gly Phe His Ser His Val
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 160 165 170
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 Val Met Lys Asn Gly Glu Leu Leu Gln Ile Lys Ser Asn His Arg Asp
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10294.000.ST25.txt

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Asp	Lys	Asn	Glu	Ile	Tyr	Val	Leu	Cys	Met	Glu	Glu	Asp	Ile	Met	Lys	
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Val	Val	Asn	Leu	Leu	Met	Glu	Asn	Lys	Ile	Arg	Val	Leu	His	Met	Lys	
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Gln	Glu	Lys	Gln	Ser	Ile	Glu	Gln	Ser	Phe	Leu	Glu	Leu	Ile	Asn	Lys	
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Thr	Ile	Phe	Gly	Leu	Leu	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Thr	Thr	Leu
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Val Gly Ser Val Val Glu Asn Pro Ser Phe Tyr Glu His Leu Thr Gly
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Tyr Gln Asn Leu Lys Tyr Leu Gly Gly Phe His Ser His Val Ser Lys
100 105 110

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115 120 125

His Lys Pro Val Lys Thr Tyr Ser Leu Gly Met Lys Gln Arg Leu Gly
130 135 140

Leu Ala Val Ala Leu Leu His Asp Pro Glu Phe Leu Ile Leu Asp Glu
145 150 155 160

Pro Thr Asn Gly Leu Asp Pro Gln Gly Ile Ile Asp Leu Arg Glu His
165 170 175

Leu Gln Tyr Leu Ala Lys Thr Phe Asn Lys Thr Ile Leu Ile Ser Ser
180 185 190

His Leu Leu Ser Glu Val Glu Met Ile Cys Asp Glu Tyr Gly Val Met
195 200 205

Lys Asn Gly Glu Leu Leu Gln Ile Lys Ser Asn His Arg Asp Thr Asp
210 215 220

Thr Val Arg Tyr Arg Leu Thr Leu Asn Gly His Ala Asp Glu Ala Ala
225 230 235 240

Asp Leu Leu Asn Glu Tyr Gln Tyr Ala Gly Gly Leu Thr Glu Asp Lys
245 250 255

Asn Glu Ile Tyr Val Leu Cys Met Glu Glu Asp Ile Met Lys Val Val
260 265 270

Asn Leu Leu Met Glu Asn Lys Ile Arg Val Leu His Met Lys Gln Glu
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Lys Thr Lys Lys Val Ser Gly Tyr Ile Thr Trp Tyr Asn Gly Val Gly
30 35 40

aaa atc ggc gct gac ggc aag agg ctc ggc cat tgg gac tgc gcc aca 677
Lys Ile Gly Ala Asp Gly Lys Arg Leu Gly His Trp Asp Cys Ala Thr
45 50 55

aag atg ggc ttc gat gtt ccg aga aaa ggc aca aaa ata aga gcc tat 725
Lys Met Gly Phe Asp Val Pro Arg Lys Gly Thr Lys Ile Arg Ala Tyr
60 65 70

tca aaa gca aaa ccg cac aaa gtc att aca gtc tat aaa tat gat gtc 773
Ser Lys Ala Lys Pro His Lys Val Ile Thr Val Tyr Lys Tyr Asp Val
80 85 90

ggc aga atg ccg ggc gct gtt ttg gat gta agc ccg aaa gct ttt aga 821
Gly Arg Met Pro Gly Ala Val Leu Asp Val Ser Pro Lys Ala Phe Arg
95 100 105

gct ttg gga ttt ccg aca agc aaa gga aag gta gcc gga cat tat aca 869
Ala Leu Gly Phe Pro Thr Ser Lys Gly Lys Val Ala Gly His Tyr Thr
110 115 120

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Tyr Lys Lys
125

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<210> 86

<211> 126

<212> PRT

<213> Bacillus licheniformis

<400> 86

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Leu Ala Phe Asn Phe Ala Gly Glu Ala Ser Ala Lys Thr Lys Lys Val
20 25 30

Ser Gly Tyr Ile Thr Trp Tyr Asn Gly Val Gly Lys Ile Gly Ala Asp
35 40 45

Gly Lys Arg Leu Gly His Trp Asp Cys Ala Thr Lys Met Gly Phe Asp
50 55 60

Val Pro Arg Lys Gly Thr Lys Ile Arg Ala Tyr Ser Lys Ala Lys Pro
65 70 75 80

His Lys Val Ile Thr Val Tyr Lys Tyr Asp Val Gly Arg Met Pro Gly
85 90 95

Ala Val Leu Asp Val Ser Pro Lys Ala Phe Arg Ala Leu Gly Phe Pro
100 105 110

Thr Ser Lys Gly Lys Val Ala Gly His Tyr Thr Tyr Lys Lys
115 120 125

<210> 87

<211> 1957

<212> DNA

10294.000.ST25.txt

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ttt Phe	aat Asn	caa Gln	aaa Lys 175	atg Met	aaa Lys	gcc Ala	gcc Ala	cgc Arg 180	gcg Ala	aaa Lys	att Ile	aaa Lys	gat Asp 185	gca Ala	tct Ser	1061
gta Val	aaa Lys	ggt Gly 190	gaa Glu	acg Thr	ttc Phe	tct Ser	tta Leu 195	atc Ile	ggc Gly	gca Ala	tat Tyr	gca Ala 200	aaa Lys	tct Ser	tta Leu	1109
tat Tyr	gtc Val 205	tac Tyr	ggg Gly	gca Ala	tac Tyr	ggg Gly 210	tat Tyr	cgg Arg	ggc Gly	gga Gly	gaa Glu 215	gcg Ala	atc Ile	tat Tyr	acg Thr	1157
cag Gln 220	ctg Leu	gga Gly	ctg Leu	acg Thr	ccg Pro 225	cct Pro	gaa Glu	tct Ser	gtt Val	aaa Lys 230	aag Lys	gat Asp	gcc Ala	att Ile	gat Asp 235	1205
aca Thr	gct Ala	gac Asp	gga Gly	tat Tyr 240	aaa Lys	gcc Ala	ata Ile	tct Ser	ttc Phe 245	gag Glu	gtc Val	ctg Leu	ccg Pro	aaa Lys 250	tat Tyr	1253
gcc Ala	gga Gly	gac Asp	tac Tyr 255	ata Ile	ttt Phe	gtc Val	gac Asp	gaa Glu 260	tca Ser	tac Tyr	aac Asn	gga Gly	aag Lys 265	ctt Leu	gat Asp	1301
cag Gln	gac Asp	aat Asn 270	ccg Pro	gtt Val	tgg Trp	gca Ala	tcg Ser 275	ctt Leu	gac Asp	gcg Ala	gtg Val	aaa Lys 280	aaa Lys	ggc Gly	aag Lys	1349
gtc Val	ttt Phe 285	ttc Phe	ctc Leu	gat Asp	ccg Pro	gac Asp 290	aga Arg	ttt Phe	tgg Trp	ccg Pro	tat Tyr 295	gat Asp	cca Pro	aac Asn	gct Ala	1397
gtt Val 300	cag Gln	gca Ala	cag Gln	gcc Ala	gaa Glu 305	gaa Glu	atc Ile	gcc Ala	gac Asp	atg Met 310	att Ile	tcc Ser	aag Lys	aaa Lys	gcg Ala 315	1445
aaa Lys	aat Asn	aaa Lys	tagaaaagcg	gggagccgaa	aagaatgatc	cggcttcccg										1494
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cccgcatctt	ggatggggat	gatataggcg	gcttcatctg	actcattatg	gtgggaatgc											1614
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ggaggcacga	tgccgaacat	tgcccacaat	acatgggtga	tcgtcagcgt	ttgatcgaat											1854
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<210> 88

<211> 318

<212> PRT

<213> Bacillus licheniformis

<400> 88

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 Glu Lys Asn Glu Glu Lys Thr Arg Val Val Lys Thr Ile Asn Gly Asn
 35 40 45
 Val Thr Val Pro Ala Asn Pro Lys Arg Val Val Thr Ile Gly Tyr Ala
 50 55 60
 Gly Thr Met Leu Ala Phe Gly Ile Lys Pro Leu Gly Glu Thr Gly Lys
 65 70 75 80
 Tyr Leu Gly Ser Pro Tyr Ile Lys Asp Gln Val Ser Gly Ile Lys Asp
 85 90 95
 Ile Gly Gly Lys Asp Gly Phe Ser Val ser Val Glu Lys Val Leu Glu
 100 105 110
 Leu Lys Pro Asp Leu Ile Val ser Met Thr Asn Asp Ser Lys Glu Tyr
 115 120 125
 Glu Lys Leu Ser Lys Ile Ala Pro Thr Val Val Tyr Pro Phe Gly Thr
 130 135 140
 Phe Lys Asp Ala Arg Asp Glu Met Lys Thr Phe Gly Lys Leu Leu Gly
 145 150 155 160
 Lys Glu Lys Glu Ala Arg Glu Trp Thr Lys Thr Phe Asn Gln Lys Met
 165 170 175
 Lys Ala Ala Arg Ala Lys Ile Lys Asp Ala Ser Val Lys Gly Glu Thr
 180 185 190
 Phe ser Leu Ile Gly Ala Tyr Ala Lys Ser Leu Tyr Val Tyr Gly Ala
 195 200 205
 Tyr Gly Tyr Arg Gly Gly Glu Ala Ile Tyr Thr Gln Leu Gly Leu Thr
 210 215 220
 Pro Pro Glu Ser Val Lys Lys Asp Ala Ile Asp Thr Ala Asp Gly Tyr
 225 230 235 240

10294.000.ST25.txt

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 Glu Val Val Glu Ser Ser Val Glu Val Ala Glu Ile Thr Thr Asn Leu
 45 50 55
 aaa tca gac aat gta gtc cgt ttg tca atc aag ctt gaa acc gat tcg 725
 Lys Ser Asp Asn Val Val Arg Leu Ser Ile Lys Leu Glu Thr Asp Ser
 60 65 70 75
 aaa gag gcg aaa gaa gag ctt gaa aag cgg gat ttc caa att aaa gat 773
 Lys Glu Ala Lys Glu Glu Leu Glu Lys Arg Asp Phe Gln Ile Lys Asp
 80 85 90
 tca gtc atc tcc ctt ttg gcg aac acg aac gca gat gag ctt gaa gga 821
 Ser Val Ile Ser Leu Leu Ala Asn Thr Asn Ala Asp Glu Leu Glu Gly
 95 100 105
 caa aaa gga aaa gaa aaa ttt aaa gaa cag ctg aaa gaa aag ctg aac 869
 Gln Lys Gly Lys Glu Lys Phe Lys Glu Gln Leu Lys Glu Lys Leu Asn
 110 115 120
 acg aac tac atg aaa gag gga aaa gtg aaa act gtg tac att acc tcc 917
 Thr Asn Tyr Met Lys Glu Gly Lys Val Lys Thr Val Tyr Ile Thr Ser
 125 130 135
 ttt aat ctg cag taggaacata gatgacagaa ccatggaggt gaaaacagat 969
 Phe Asn Leu Gln
 140
 ggcaggagaa gtgctctccc aaaatgaaat cgatgcactg ctttcagcga tatcgaccgg 1029
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 ctttaaaccgg gcgctccgct tttcaaagga tcaaatccgc agcttgacca ggattcacga 1149
 taactttgca aggctgctaa cgacttattt ctcagctcag ttgagaacct atatccaaat 1209
 ctcggtcagc tcggttgatc aggttccgta tgaggaattc atcagatcga ttccgaatat 1269
 gacgatcctc aatctgtttg aggttcgccc tcttgaagga agaatcatga tggagatcaa 1329
 cccgaccatc gcctatacga tgatggaccg ggtgatgggc gggatcggct cgagccacaa 1389
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<210> 90

<211> 143

<212> PRT

<213> Bacillus licheniformis

<400> 90

Met Asn Lys Lys Leu Leu Gly Ile Met Met Thr Ile Ile Leu Ala Ile
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Ala Val Leu Gly Thr Ala Ala Phe Phe Val Ile Lys Gly Ser Ala Ser
 20 25 30

Glu Lys Asp Gln Asn Ala Glu Pro Ser Ile Asp Glu Val Val Glu Ser
 35 40 45

10294.000.ST25.txt

Ser Val Glu Val Ala Glu Ile Thr Thr Asn Leu Lys Ser Asp Asn Val
50 55 60
Val Arg Leu Ser Ile Lys Leu Glu Thr Asp Ser Lys Glu Ala Lys Glu
65 70 75 80
Glu Leu Glu Lys Arg Asp Phe Gln Ile Lys Asp Ser Val Ile Ser Leu
85 90 95
Leu Ala Asn Thr Asn Ala Asp Glu Leu Glu Gly Gln Lys Gly Lys Glu
100 105 110
Lys Phe Lys Glu Gln Leu Lys Glu Lys Leu Asn Thr Asn Tyr Met Lys
115 120 125
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130 135 140

<210> 91

<211> 1366

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (488)..(874)

<223>

<400> 91
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cagaatgaat gtcggatgtt cgctctctgt tgtaaaaagac ggactccgac gtctgaagac 180
cgcttttttcg taagcggttc ggctgaaaagc cgggcgcttc taagagcggt tatggatggt 240
ttcattcaat tctctttcca gcttttccgc tttttcagct tcttttttgg aatgcttgat 300
aatcagcccg aatacagcga tcgcgatgat aaagaaaaacg gccagcgtaa taaaagaagg 360
gatatatctt cttttgtctt caggaaaata gagcataaac tgaatcagaa acggcgccat 420
ttttcttcct ccctgaaatg atttttttac catttattta ttatgatacc attaggaggc 480
agatgca gtg aac aac caa ttt caa gtc gga gat cgc gta aag ggc ttt 529
Val Asn Asn Gln Phe Gln Val Gly Asp Arg Val Lys Gly Phe
1 5 10
tat aaa aca ggc gtc tac atc ggc gaa att acg gat gtt aaa ccg atg 577

10294.000.ST25.txt

Tyr Lys Thr Gly Val Tyr Ile Gly Glu Ile Thr Asp Val Lys Pro Met
 15 20 25 30
 cac tac ctg gtc aaa atc ctc gcc gtg ctg acc cat ccg aag cag ggc 625
 His Tyr Leu Val Lys Ile Leu Ala Val Leu Thr His Pro Lys Gln Gly
 35 40 45
 gac ctt cat cat ccc aat cgg gca gac gtc cct ttt ttt cat gaa cga 673
 Asp Leu His His Pro Asn Arg Ala Asp Val Pro Phe Phe His Glu Arg
 50 55 60
 aaa gcg ctc gct tac ggt gaa cag acg aat atc ccg cac cgc atg gtg 721
 Lys Ala Leu Ala Tyr Gly Glu Gln Thr Asn Ile Pro His Arg Met Val
 65 70 75
 aag ccg ttc gat gaa gct gta ccg gat tat gcg gat tcg ctc cgc tca 769
 Lys Pro Phe Asp Glu Ala Val Pro Asp Tyr Ala Asp Ser Leu Arg Ser
 80 85 90
 gct ttg agc cgc tta aaa acg gat ctg caa aac gat tcg tcc gaa tac 817
 Ala Leu Ser Arg Leu Lys Thr Asp Leu Gln Asn Asp Ser Ser Glu Tyr
 95 100 105 110
 gcg gca aaa tcg ctt gag ctt att cat ggg ctt gaa aaa gaa tat ttc 865
 Ala Ala Lys Ser Leu Glu Leu Ile His Gly Leu Glu Lys Glu Tyr Phe
 115 120 125
 ctg cac aaa taacccaatc tgtttgcag attgggtttt ttatgtggcg 914
 Leu His Lys
 tgccgaaaga cttttgagag gtcaacccgt tcgccgatcg tcgtcggctt cggattttcc 974
 aaatacttct tatcccggtc tacgagccga aacaacttat acgttgtcat cgcgtcgtca 1034
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 <210> 92
 <211> 129
 <212> PRT
 <213> Bacillus licheniformis
 <400> 92
 Val Asn Asn Gln Phe Gln Val Gly Asp Arg Val Lys Gly Phe Tyr Lys
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 Thr Gly Val Tyr Ile Gly Glu Ile Thr Asp Val Lys Pro Met His Tyr
 20 25 30

Leu Val Lys Ile Leu Ala Val Leu Thr His Pro Lys Gln Gly Asp Leu
 35 40 45

His His Pro Asn Arg Ala Asp Val Pro Phe Phe His Glu Arg Lys Ala
 50 55 60

Leu Ala Tyr Gly Glu Gln Thr Asn Ile Pro His Arg Met Val Lys Pro
 65 70 75 80

Phe Asp Glu Ala Val Pro Asp Tyr Ala Asp Ser Leu Arg Ser Ala Leu
 85 90 95

Ser Arg Leu Lys Thr Asp Leu Gln Asn Asp Ser Ser Glu Tyr Ala Ala
 100 105 110

Lys Ser Leu Glu Leu Ile His Gly Leu Glu Lys Glu Tyr Phe Leu His
 115 120 125

Lys

<210> 93

<211> 1909

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1406)

<223>

<400> 93
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 ctgaaaacgg agaaagcatg gagatccgcg gccgcgatct tttacaggc ctgccgaaaa 180
 cgattgaaat cactgaaaaa gaaattacag cggctcttcg cgacactgtg accgccattg 240
 tcgatgccgt aaaaaatacg cttagaaaaa ctccgcctga actcgcggct gatattatgg 300
 accgcggaat cgtccttacg ggaggcggcg cactgctgcg ccacctggac aaagtcatca 360
 gcgaagaaac gaaaatgccg gttttaattg cggaagaccc tcttgactgt gtagcgatcg 420
 gaacaggcaa agctctcgag caaattcatc tatttaaagg caaaaattaa ggacacaggg 480
 aatagaagag gtgtataatc atg ccg cag ttt ttt aca aat aaa cgg ttg atg 533
 Met Pro Gln Phe Phe Thr Asn Lys Arg Leu Met
 1 5 10

10294.000.ST25.txt

ctt tta ctc ctt tgt atc atc att tta gtg gca atg att gga ttt tcg Leu Leu Leu 15 Leu Cys Ile Ile Ile Leu Val Ala Met Ile 25 Gly Phe Ser	581
tta aag aat gac cgg aat gca act tgg ccc gaa aaa ttt att ggc gat Leu Lys Asn 30 Asp Arg Asn Ala Thr 35 Trp Pro Glu Lys 40 Phe Ile Gly Asp	629
aca act ggt gta ttc cag acg att ttt cat acg ccc gct caa ttt ttt Thr Thr 45 Gly Val Phe Gln Thr 50 Ile Phe His Thr 55 Pro Ala Gln Phe Phe	677
gcg ggc ttc ttt gaa aat atc gaa gac tta aaa aat acg tac agc gaa Ala Gly Phe Phe Glu Asn 65 Ile Glu Asp Leu Lys 70 Asn Thr Tyr Ser Glu 75	725
aat gag cgc ctg cgg aaa aag ctc gac ggc cag aca caa tac gag gca Asn Glu Arg Leu 80 Arg Lys Lys Leu Asp Gly 85 Gln Thr Gln Tyr Glu Ala	773
aag ctg cag gag ctt gaa aat gaa aat aag tct tta aga aaa gag ctc Lys Leu Gln 95 Glu Leu Glu Asn Glu Asn 100 Lys Ser Leu Arg Lys 105 Glu Leu	821
ggc cat ctg aaa tca att aaa gac tac acg ccg att ctg gcg acc gtt Gly His 110 Leu Lys Ser Ile Lys Asp 115 Tyr Thr Pro Ile Leu 120 Ala Thr Val	869
atc gcc aga aat ccc gat aag tat gag tgg tgg aac ctg att acg atc Ile Ala Arg Asn Pro Asp Lys 130 Tyr Glu Trp Trp Asn 135 Leu Ile Thr Ile	917
aac aaa ggt tca aag cac ggc gtt gag aag gat atg gcg gta aca gat Asn Lys Gly Ser Lys 145 His Gly Val Glu Lys Asp 150 Met Ala Val Thr Asp 155	965
gaa aac ggc aac ttg atc gga aaa atc aaa agc aca aaa gtg aac aat Glu Asn Gly Asn 160 Leu Ile Gly Lys Ile Lys 165 Ser Thr Lys Val Asn Asn 170	1013
ttc act tcc acc gtc cag ctt tta agc gca aca gac aga aac aac aga Phe Thr Ser 175 Val Gln Leu Leu Ser 180 Ala Thr Asp Arg 185 Asn Asn Arg	1061
atc tcc aca gtt atc gct gca gat aaa ggc aag aaa acg gtg aac gga Ile Ser Thr 190 Val Ile Ala Ala Asp 195 Lys Gly Lys Lys Thr 200 Val Asn Gly	1109
atc atc aac ggc tac gac tca gat aaa aag gcg ctt tcc atg gaa atc Ile Ile Asn Gly Tyr Asp Ser 210 Lys Lys Ala Leu 215 Ser Met Glu Ile	1157
atc gag cct gat gaa gac agg gaa gtg aaa aaa ggt gac ctc gtc gaa Ile Glu Pro Asp Glu Asp 225 Arg Glu Val Lys Lys 230 Gly Asp Leu Val Glu 235	1205
act tcc ggt gcg ggc ggc gtt ttt cct aaa ggc ctg aca atc gga aaa Thr Ser Gly Ala 240 Gly Gly Val Phe Pro Lys 245 Gly Leu Thr Ile Gly Lys 250	1253
gtg aca gag gtt gaa cca gat tcc tac ggt ttg acg aaa atc gct tat Val Thr Glu Val 255 Glu Pro Asp Ser Tyr 260 Gly Leu Thr Lys 265 Ile Ala Tyr	1301
gta gag ccg gca gcc gat atg tat aac ctt gat aac gtc atc gtc gtc Val Glu Pro 270 Ala Ala Asp Met Tyr 275 Asn Leu Asp Asn Val 280 Ile Val Val	1349

10294.000.ST25.txt

gac aga acg ctt gat acg gtg gat gtc gac aag atg gac gat gag gag 1397
 Asp Arg Thr Leu Asp Thr Val Asp Val Asp Lys Met Asp Asp Glu Glu
 285 290 295

gaa ggg tcg tgaaacgctt cttcttccc gtcgtcatga tgtttgtttt 1446
 Glu Gly Ser
 300

agtatctgac agcgtctatg cggattttgt caacttgcct tttgtgacgg aagaacagca 1506
 gctcatcccg cgttttctgc tgcttgctt agtttttatg acggcttatg tcaatcagcc 1566
 ttttgccatt acatatggat ttattttcgg actgttatat gatattaatt acaccgacct 1626
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 tgaattttac caatatggcg tgcagatgct gatacgtccg gaaattatgc cgttccatca 1806
 atttgtgctc ggcaggctcc tgcccacgct tgcgtgaac gccgttgggc gccttctgct 1866
 catttacccg ttcaaattggg tttttaccag tcttaagaaa gag 1909

<210> 94

<211> 302

<212> PRT

<213> Bacillus licheniformis

<400> 94

Met Pro Gln Phe Phe Thr Asn Lys Arg Leu Met Leu Leu Leu Leu Cys
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Ile Ile Ile Leu Val Ala Met Ile Gly Phe Ser Leu Lys Asn Asp Arg
 20 25 30

Asn Ala Thr Trp Pro Glu Lys Phe Ile Gly Asp Thr Thr Gly Val Phe
 35 40 45

Gln Thr Ile Phe His Thr Pro Ala Gln Phe Phe Ala Gly Phe Phe Glu
 50 55 60

Asn Ile Glu Asp Leu Lys Asn Thr Tyr Ser Glu Asn Glu Arg Leu Arg
 65 70 75 80

Lys Lys Leu Asp Gly Gln Thr Gln Tyr Glu Ala Lys Leu Gln Glu Leu
 85 90 95

Glu Asn Glu Asn Lys Ser Leu Arg Lys Glu Leu Gly His Leu Lys Ser
 100 105 110

Ile Lys Asp Tyr Thr Pro Ile Leu Ala Thr Val Ile Ala Arg Asn Pro
 115 120 125

10294.000.ST25.txt

Asp Lys Tyr Glu Trp Trp Asn Leu Ile Thr Ile Asn Lys Gly Ser Lys
 130 135 140
 His Gly Val Glu Lys Asp Met Ala Val Thr Asp Glu Asn Gly Asn Leu
 145 150 155 160
 Ile Gly Lys Ile Lys Ser Thr Lys Val Asn Asn Phe Thr Ser Thr Val
 165 170 175
 Gln Leu Leu Ser Ala Thr Asp Arg Asn Asn Arg Ile Ser Thr Val Ile
 180 185 190
 Ala Ala Asp Lys Gly Lys Lys Thr Val Asn Gly Ile Ile Asn Gly Tyr
 195 200 205
 Asp Ser Asp Lys Lys Ala Leu Ser Met Glu Ile Ile Glu Pro Asp Glu
 210 215 220
 Asp Arg Glu Val Lys Lys Gly Asp Leu Val Glu Thr Ser Gly Ala Gly
 225 230 235 240
 Gly Val Phe Pro Lys Gly Leu Thr Ile Gly Lys Val Thr Glu Val Glu
 245 250 255
 Pro Asp Ser Tyr Gly Leu Thr Lys Ile Ala Tyr Val Glu Pro Ala Ala
 260 265 270
 Asp Met Tyr Asn Leu Asp Asn Val Ile Val Val Asp Arg Thr Leu Asp
 275 280 285
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 290 295 300

<210> 95

<211> 1450

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (121)..(951)

<223>

<400> 95
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 Page 186

10294.000.ST25.txt

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atg aca cat agc gca tta aag cat tta gat tat cac aat tgg gcg aat Met Thr His Ser Ala Leu Lys His Leu Asp Tyr His Asn Trp Ala Asn 1 5 10 15	168
caa agg gtg ctc acc cac ctg aaa agc ctg cct gaa gag ctg ttc acc Gln Arg Val Leu Thr His Leu Lys Ser Leu Pro Glu Glu Leu Phe Thr 20 25 30	216
cgg gaa atc aaa agc gtt ttt caa act gta tct gag gtt gtt acc cat Arg Glu Ile Lys Ser Val Phe Gln Thr Val Ser Glu Val Val Thr His 35 40 45	264
atg tgc ggc gct gac gac ctt agg ctg aaa gat acc acc ctc tta acc Met Cys Gly Ala Asp Asp Leu Arg Leu Lys Asp Thr Thr Leu Leu Thr 50 55 60	312
aga aag tgt ggg gga aag tat acc cgc aga acc gtt caa aaa atg aag Arg Lys Cys Gly Gly Lys Tyr Thr Arg Arg Thr Val Gln Lys Met Lys 65 70 75 80	360
cca aag ttt agg ttg cag tgt cag ttt aag aag aag cgc caa aag tac Pro Lys Phe Arg Leu Gln Cys Gln Phe Lys Lys Lys Arg Gln Lys Tyr 85 90 95	408
att tgt ggt gaa agg aat aat att ggg cgg aac act gtc aat ggt aat Ile Cys Gly Glu Arg Asn Asn Ile Gly Arg Asn Thr Val Asn Gly Asn 100 105 110	456
ttt aaa gca agc cga ttt aat gaa aaa tgg gta acc gac att acc tac Phe Lys Ala Ser Arg Phe Asn Glu Lys Trp Val Thr Asp Ile Thr Tyr 115 120 125	504
tta cat tat ggc tcc gat atg tta tat tta tca acg att atg gac tta Leu His Tyr Gly Ser Asp Met Leu Tyr Leu Ser Thr Ile Met Asp Leu 130 135 140	552
tat aac aac gaa ata gtg gct tac aaa ata ggt acg agc caa gat att Tyr Asn Asn Glu Ile Val Ala Tyr Lys Ile Gly Thr Ser Gln Asp Ile 145 150 155 160	600
aac cta gta tta gac aca ttg agg gaa gct gta gaa tta cgt aaa cca Asn Leu Val Leu Asp Thr Leu Arg Glu Ala Val Glu Leu Arg Lys Pro 165 170 175	648
gta ggg tta ctt ctt cat agc gac cag gga tct gtc tat act tca cat Val Gly Leu Leu Leu His Ser Asp Gln Gly Ser Val Tyr Thr Ser His 180 185 190	696
gca tat cag aat ttg gcc aaa gaa aaa ggc att acc aca agc atg tct Ala Tyr Gln Asn Leu Ala Lys Glu Lys Gly Ile Thr Thr Ser Met Ser 195 200 205	744
cga aaa gga aac tgc cat gat aat gcc gtc att gaa tcc ttt cac tcc Arg Lys Gly Asn Cys His Asp Asn Ala Val Ile Glu Ser Phe His Ser 210 215 220	792
tcg cta aag tcg gaa gga ttt aac gct caa agt aga gca tct ata tcc Ser Leu Lys Ser Glu Gly Phe Asn Ala Gln Ser Arg Ala Ser Ile Ser 225 230 235 240	840
aat tct aaa gta gta caa att gta aat caa tac atg tat cga tat aat Asn Ser Lys Val Val Gln Ile Val Asn Gln Tyr Met Tyr Arg Tyr Asn 245 250 255	888
cat gta cga att cag gca aaa tta aac tac ctg tcc cca ctg gaa tac	936

His Val Arg Ile Gln Ala Lys Leu Asn Tyr Leu Ser Pro Leu Glu Tyr
 260 265 270

agg gga cag gca gca taggtgtttt ttctaagtct cattttaacg ggtcagttca 991
 Arg Gly Gln Ala Ala
 275

tctttacatg ccgggttttt gctttattca ggctgcttcg cgtccgcttc aagccggggcc 1051
 actgctccag gcgacgcttt ttccaccgct ctggcggcta tgctgtaagc ctcttcatac 1111
 tgatatgctg aaaaacagtt ttctgcttct ttcagctgtt cggaaaggat acggtccttg 1171
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 tcgtccgtct ttgttttcac ttccgtgaca agctgttccg cctcttgaag acgttcgttc 1291
 accgcatcca tgttcagcgg cagctcattc aactgttctg tcactttctg cacagtcgtc 1351
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<210> 96

<211> 277

<212> PRT

<213> Bacillus licheniformis

<400> 96

Met Thr His Ser Ala Leu Lys His Leu Asp Tyr His Asn Trp Ala Asn
 1 5 10 15

Gln Arg Val Leu Thr His Leu Lys Ser Leu Pro Glu Glu Leu Phe Thr
 20 25 30

Arg Glu Ile Lys Ser Val Phe Gln Thr Val Ser Glu Val Val Thr His
 35 40 45

Met Cys Gly Ala Asp Asp Leu Arg Leu Lys Asp Thr Thr Leu Leu Thr
 50 55 60

Arg Lys Cys Gly Gly Lys Tyr Thr Arg Arg Thr Val Gln Lys Met Lys
 65 70 75 80

Pro Lys Phe Arg Leu Gln Cys Gln Phe Lys Lys Lys Arg Gln Lys Tyr
 85 90 95

Ile Cys Gly Glu Arg Asn Asn Ile Gly Arg Asn Thr Val Asn Gly Asn
 100 105 110

Phe Lys Ala Ser Arg Phe Asn Glu Lys Trp Val Thr Asp Ile Thr Tyr
 115 120 125

10294.000.ST25.txt

Leu His Tyr Gly Ser Asp Met Leu Tyr Leu Ser Thr Ile Met Asp Leu
130 135 140

Tyr Asn Asn Glu Ile Val Ala Tyr Lys Ile Gly Thr Ser Gln Asp Ile
145 150 155 160

Asn Leu Val Leu Asp Thr Leu Arg Glu Ala Val Glu Leu Arg Lys Pro
165 170 175

Val Gly Leu Leu Leu His Ser Asp Gln Gly Ser Val Tyr Thr Ser His
180 185 190

Ala Tyr Gln Asn Leu Ala Lys Glu Lys Gly Ile Thr Thr Ser Met Ser
195 200 205

Arg Lys Gly Asn Cys His Asp Asn Ala Val Ile Glu Ser Phe His Ser
210 215 220

Ser Leu Lys Ser Glu Gly Phe Asn Ala Gln Ser Arg Ala Ser Ile Ser
225 230 235 240

Asn Ser Lys Val Val Gln Ile Val Asn Gln Tyr Met Tyr Arg Tyr Asn
245 250 255

His Val Arg Ile Gln Ala Lys Leu Asn Tyr Leu Ser Pro Leu Glu Tyr
260 265 270

Arg Gly Gln Ala Ala
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<210> 97

<211> 2312

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1925)

<223>

<400> 97
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aaagaagaaa ttgcacgggc aaaagcggcg ttcaaaaga aaatcaatag gaagccggag 120
cttaaacagg acaagagcga atcggttaaat aaggaaatca tgaggctcta ctttaacggg 180
ggaaaaaaga agaagccttag agctgttgat ttcgtcggaa cgattgctaa aattgacggc 240

10294.000.ST25.txt

cct Pro	gaa Glu	aca Thr	cag Gln	tat Tyr 240	tac Tyr	tac Tyr	ctg Leu	tac Tyr	atg Met 245	tcc Ser	ttc Phe	ggg Gly	ggg Gly	ctt Leu 250	gcc Ala	1253
gct Ala	gac Asp	ggg Gly	ggt Gly 255	tac Tyr	aac Asn	att Ile	cgc Arg	gtc Val 260	gcc Ala	cgc Arg	tcc Ser	aaa Lys	aac Asn 265	cct Pro	gac Asp	1301
ggg Gly	cct Pro	tat Tyr 270	tat Tyr	gat Asp	gca Ala	gaa Glu	ggc Gly 275	cac His	gcg Ala	atg Met	att Ile	gac Asp 280	gtc Val	cgc Arg	ggc Gly	1349
aaa Lys	gaa Glu 285	gga Gly	acg Thr	ctt Leu	ttt Phe	gac Asp 290	gat Asp	cgt Arg	tca Ser	atc Ile	gaa Glu 295	ccg Pro	tac Tyr	ggc Gly	gtc Val	1397
aaa Lys 300	ctg Leu	atg Met	gga Gly	aat Asn	ttc Phe 305	tca Ser	ttt Phe	aac Asn	aat Asn	aaa Lys 310	aac Asn	ggc Gly	tat Tyr	gtg Val	tcg Ser 315	1445
ccg Pro	ggc Gly	cat His	aac Asn	tct Ser 320	gcc Ala	ttt Phe	tac Tyr	gat Asp	gaa Glu 325	aaa Lys	agc Ser	ggt Gly	aaa Lys	tca Ser 330	tat Tyr	1493
tta Leu	atc Ile	ttc Phe	cac His 335	acc Thr	cgc Arg	ttc Phe	ccg Pro	gga Gly 340	cgg Arg	ggc Gly	gag Glu	gag Glu	cac His 345	gaa Glu	gtc Val	1541
cgc Arg	gtc Val	cac His 350	caa Gln	ttg Leu	ctg Leu	atg Met	aac Asn 355	aaa Lys	caa Gln	ggc Gly	tgg Trp	ccg Pro 360	gtt Val	gtc Val	gcc Ala	1589
cct Pro	cac His 365	cgc Arg	tat Tyr	gcc Ala	gga Gly	gag Glu 370	aag Lys	ctt Leu	gaa Glu	aag Lys	gtg Val 375	aaa Lys	aag Lys	tca Ser	gat Asp	1637
gtg Val 380	att Ile	ggc Gly	gat Asp	tac Tyr	gaa Glu 385	ttg Leu	gtg Val	agg Arg	cac His	ggc Gly 390	aaa Lys	gac Asp	atc Ile	tcc Ser	gca Ala 395	1685
gat Asp	att Ile	aaa Lys	gaa Glu	tcg Ser 400	aaa Lys	gaa Glu	atc Ile	cgc Arg	ttg Leu 405	aat Asn	caa Gln	aat Asn	ggc Gly	aaa Lys 410	ata Ile	1733
aca Thr	ggc Gly	gca Ala	gta Val 415	gcc Ala	gga Gly	acg Thr	tgg Trp	aag Lys 420	aac Asn	acg Thr	ggg Gly	cat His	aac Asn 425	aaa Lys	ata Ile	1781
gaa Glu	ctc Leu	aag Lys 430	atc Ile	gac Asp	gga Gly	aaa Lys	acc Thr 435	tac Tyr	gat Asp	ggc Gly	gtg Val	ttt Phe 440	ttg Leu	cgt Arg	cag Gln	1829
tgg Trp	gat Asp 445	gcg Ala	gct Ala	tct Ser	gag Glu	cgt Arg 450	aag Lys	gtg Val	atg Met	acg Thr	ttt Phe 455	agt Ser	gcg Ala	ttg Leu	tct Ser	1877
cgt Arg 460	gag Glu	gga Gly	gat Asp	gcg Ala	gtt Val 465	tgg Trp	ggg Gly	agt Ser	agt Ser	tta Leu 470	aaa Lys	aga Arg	gcg Ala	gaa Glu	ttt Phe 475	1925
taaaaggaat ttcattctta aaagcacatt cctgattaaa ggtatgtgct ttttaaataga																1985
tttagatcaa atggttgttt taatatggaa attcaggatg gattatacga taatacatat																2045
atgggtctttt ttactacata agttgttcgt gagattctat gaagaaaaat caacaagggg																2105
tgttgataaaa atgggtttta aaaggagttt taaaataatg cctggtgtca aacttaatat																2165

10294.000.ST25.txt

aaataaaaaa agtggtggga tgactttagg gggcaaaaat ggcaggataa cttataatac 2225
 ttctggcaaa gtaacaacaa gtgcaaaaat ccccggtaca ggtctatctt atagttccag 2285
 taaatctatt tcttcacac aaaaaca 2312

<210> 98

<211> 475

<212> PRT

<213> Bacillus licheniformis

<400> 98

Met Asn Met Arg Lys Cys Phe Ile Gln Val Leu Ala Leu Leu Phe Ile
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Ile Ala Ala Cys Phe Ala Pro Asn Gln Ala Ser Ala Gln Thr Gln Lys
 20 25 30

Pro Val Phe Ser Glu Val Thr Val His Asp Pro Ser Ile Ile Lys Ala
 35 40 45

Asn Gly Thr Tyr Tyr Val Phe Gly Ser His Leu Ala Ser Ala Lys Ser
 50 55 60

Thr Asp Leu Met Asn Trp Thr Gln Ile Ser Ser Ser Val His Asp Gly
 65 70 75 80

Asn Pro Leu Ile Pro Asn Val Tyr Glu Glu Leu Lys Glu Thr Phe Glu
 85 90 95

Trp Ala Glu Ser Asp Thr Leu Trp Ala Pro Asp Val Thr Gln Leu Glu
 100 105 110

Asp Gly Lys Phe Tyr Met Tyr Tyr Asn Ala Cys Arg Gly Asp Ser Pro
 115 120 125

Arg Ser Ala Leu Gly Leu Ala Val Ala Asp Asp Ile Glu Gly Pro Tyr
 130 135 140

Lys Asn Lys Gly Ile Phe Leu Lys Ser Gly Met Asp Gly Ile Ser Asn
 145 150 155 160

Asp Gly Thr Pro Tyr Asp Ala Thr Lys His Pro Asn Val Val Asp Pro
 165 170 175

His Thr Phe Phe Asp Gln Asn Gly Lys Leu Trp Met Val Tyr Gly Ser
 180 185 190

Tyr Ser Gly Gly Ile Phe Ile Leu Glu Met Asp Lys Lys Thr Gly Phe
 195 200 205
 Pro Leu Pro Gly Gln Gly Tyr Gly Lys Lys Leu Ile Gly Gly Asn His
 210 215 220
 Ser Arg Ile Glu Gly Ala Tyr Ile Leu Tyr His Pro Glu Thr Gln Tyr
 225 230 235 240
 Tyr Tyr Leu Tyr Met Ser Phe Gly Gly Leu Ala Ala Asp Gly Gly Tyr
 245 250 255
 Asn Ile Arg Val Ala Arg Ser Lys Asn Pro Asp Gly Pro Tyr Tyr Asp
 260 265 270
 Ala Glu Gly His Ala Met Ile Asp Val Arg Gly Lys Glu Gly Thr Leu
 275 280 285
 Phe Asp Asp Arg Ser Ile Glu Pro Tyr Gly Val Lys Leu Met Gly Asn
 290 295 300
 Phe Ser Phe Asn Asn Lys Asn Gly Tyr Val Ser Pro Gly His Asn Ser
 305 310 315 320
 Ala Phe Tyr Asp Glu Lys Ser Gly Lys Ser Tyr Leu Ile Phe His Thr
 325 330 335
 Arg Phe Pro Gly Arg Gly Glu Glu His Glu Val Arg Val His Gln Leu
 340 345 350
 Leu Met Asn Lys Gln Gly Trp Pro Val Val Ala Pro His Arg Tyr Ala
 355 360 365
 Gly Glu Lys Leu Glu Lys Val Lys Lys Ser Asp Val Ile Gly Asp Tyr
 370 375 380
 Glu Leu Val Arg His Gly Lys Asp Ile Ser Ala Asp Ile Lys Glu Ser
 385 390 395 400
 Lys Glu Ile Arg Leu Asn Gln Asn Gly Lys Ile Thr Gly Ala Val Ala
 405 410 415
 Gly Thr Trp Lys Asn Thr Gly His Asn Lys Ile Glu Leu Lys Ile Asp
 420 425 430
 Gly Lys Thr Tyr Asp Gly Val Phe Leu Arg Gln Trp Asp Ala Ala Ser
 435 440 445
 Glu Arg Lys Val Met Thr Phe Ser Ala Leu Ser Arg Glu Gly Asp Ala
 450 455 460

<213> Bacillus tricheniformis

<223>

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 Gly Asn Gln Asn Glu Ile Ile Arg Leu Asp Val Pro Glu Thr Gly Arg
 110 115 120
 tac att gcg gtc gtc atg tct aaa gac ggt tca tat gac ggc tgg gga 917
 Tyr Ile Ala Val Val Met Ser Lys Asp Gly Ser Tyr Asp Gly Trp Gly
 125 130 135
 ttt tac aga ctt gaa ttt atc gac aga atg aag agc ggt gct tat acg 965
 Phe Tyr Arg Leu Glu Phe Ile Asp Arg Met Lys Ser Gly Ala Tyr Thr
 140 145 150 155
 gcg aat ttg tct ccg tca tcc atc tca agc ccg gga cag gga gtc gtt 1013
 Ala Asn Leu Ser Pro Ser Ser Ile Ser Ser Pro Gly Gln Gly Val Val
 160 165 170
 tct ccg gtt gcc gcc gtc aat ctt gcc aat gcc tcg gcc att ccc gaa 1061
 Ser Pro Val Ala Ala Val Asn Leu Ala Asn Ala Ser Ala Ile Pro Glu
 175 180 185
 gga gcg act gtg aaa agc gtt tct gcc gag gga acg ata tat cca agt 1109
 Gly Ala Thr Val Lys Ser Val Ser Ala Glu Gly Thr Ile Tyr Pro Ser
 190 195 200
 ctc gga cac acc tac aga gaa gtc ctg aac aag gaa gaa ggc gtt tgg 1157
 Leu Gly His Thr Tyr Arg Glu Val Leu Asn Lys Glu Glu Gly Val Trp
 205 210 215
 cac aca tcg gtt tca gcc gcc aca ctg ttt ccg gat cta aag cct gaa 1205
 His Thr Ser Val Ser Gly Gly Thr Leu Phe Pro Asp Leu Lys Pro Glu
 220 225 230 235
 ctt gcg ctt ccc gtc aaa acg aca tgg aat gtg aga tac tat tcg ctc 1253
 Leu Ala Leu Pro Val Lys Thr Thr Trp Asn Val Arg Tyr Tyr Ser Leu
 240 245 250
 gct tgg agc agt tca act tgg aga tcg ccg cag ctg aag atc aat tat 1301
 Ala Trp Ser Ser Ser Thr Trp Arg Ser Pro Gln Leu Lys Ile Asn Tyr
 255 260 265
 caa tac gat tca aca tac gcc tgg taaacagatc caaatcccgg ccgatataaa 1355
 Gln Tyr Asp Ser Thr Tyr Gly Trp
 270 275
 aagtaataga atgtaattgg catgaaagga gctcccatga atattagaga cagggtaaaa 1415
 ctttcgcttt attccgagca gctgatgaag ccggccgccg cgaatgtgcc ggcaaagact 1475
 aaaggctcca aaaggatgcc cgccagccaa acagacactc tctccatcag caaacaggct 1535
 gaatcagccc aaaaaaatgc accgtcatta cggtcacaaa tgaacggcgt tcaatttgag 1595
 atctataatc tttatgtgga caggcagcgt ttgaacagcc agatcgaagg ggcgctgcgg 1655
 gagagcggaa tttccctttc cgaaagcgaa catctgacat tgcattgtga cggacataac 1715
 cggattacag ttgaaggcat cgaagacgaa caaaaaagaa cccgtatcga agctgtttta 1775
 aacgacagcg ataaacgggt cggtgcgcgt ctgttgggcc acgcagaact gat 1828

 <210> 100
 <211> 275
 <212> PRT

<213> Bacillus licheniformis

<400> 100

Met Lys Lys Ser Leu Phe Leu Phe Val Phe Ser Leu Phe Leu Met Ala
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Ile Pro Ala Phe Ser Ala Ser Ala Asn Val Tyr Glu Asp Glu Tyr Glu
 20 25 30

Pro Asn Asn Ser Phe Ala Glu Ala Tyr Asp Val Gly Leu Trp Lys Tyr
 35 40 45

Lys Thr Ile Ser Ala Thr Ile His Ser Glu Ser Asp Lys Asp Tyr Tyr
 50 55 60

Lys Phe Tyr Ala Thr Lys Gly Glu Gln Leu Ala Ile His Leu Lys Asn
 65 70 75 80

Ile Pro Ala Asn Thr Asp Tyr Asp Leu Tyr Leu Phe Lys Asp Ala Tyr
 85 90 95

Gly Tyr Pro Ala Val Gly Ser Ser Glu Arg Met Gly Asn Gln Asn Glu
 100 105 110

Ile Ile Arg Leu Asp Val Pro Glu Thr Gly Arg Tyr Ile Ala Val Val
 115 120 125

Met Ser Lys Asp Gly Ser Tyr Asp Gly Trp Gly Phe Tyr Arg Leu Glu
 130 135 140

Phe Ile Asp Arg Met Lys Ser Gly Ala Tyr Thr Ala Asn Leu Ser Pro
 145 150 155 160

Ser Ser Ile Ser Ser Pro Gly Gln Gly Val Val Ser Pro Val Ala Ala
 165 170 175

Val Asn Leu Ala Asn Ala Ser Ala Ile Pro Glu Gly Ala Thr Val Lys
 180 185 190

Ser Val Ser Ala Glu Gly Thr Ile Tyr Pro Ser Leu Gly His Thr Tyr
 195 200 205

Arg Glu Val Leu Asn Lys Glu Glu Gly Val Trp His Thr Ser Val Ser
 210 215 220

Gly Gly Thr Leu Phe Pro Asp Leu Lys Pro Glu Leu Ala Leu Pro Val
 225 230 235 240

Lys Thr Thr Trp Asn Val Arg Tyr Tyr Ser Leu Ala Trp Ser Ser Ser
 245 250 255

10294.000.ST25.txt

Thr Trp Arg Ser Pro Gln Leu Lys Ile Asn Tyr Gln Tyr Asp Ser Thr
 260 265 270

Tyr Gly Trp
 275

<210> 101

<211> 2584

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (510)..(2081)

<223>

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 cttgcctact attctccatc ttcagttcag ctcatatgta cactaattta tattataata 180
 cgagtgttac gtttgcatgt caaccctatt tgcggttctt tttattctga attgattctt 240
 tggacgtcag cccagctca gtggccgttt cttccatgaa gccggcgcg cccgggtccg 300
 catgctcctt tagatgcaga ttcgcatctt gctcatggat cgccctgccc attctttgat 360
 tatacctcat gcagcaacat ccttttgata tcttttttct atagtataaa caaatcattt 420
 tcatttttatt aaaaaaacgg caaggaatat acgatataga agaagaagta gtgttccaag 480
 ttttttaccg aaaggaggag atgggaatc aat atg aaa aaa aga gcg gta ttg 533
 Asn Met Lys Lys Arg Ala Val Leu
 1 5
 atc cta tcg atg atg ctg gca gca caa gca gcc ttt tat aca tcg tca 581
 Ile Leu Ser Met Met Leu Ala Ala Gln Ala Ala Phe Tyr Thr Ser Ser
 10 15 20
 aac aca gct tct gca gcc atc ggg gaa gcc gtg att gcc acc gat gaa 629
 Asn Thr Ala Ser Ala Ala Ile Gly Glu Ala Val Ile Ala Thr Asp Glu
 25 30 35 40
 atc aat gtc aga agc ggg cct gga ctg agc cac gaa atc gtc agc gtc 677
 Ile Asn Val Arg Ser Gly Pro Gly Leu Ser His Glu Ile Val Ser Val
 45 50 55
 gtc agc agg aat gaa agc tat ccg att ctt gaa gaa cgc ggg gat tgg 725
 Val Ser Arg Asn Glu Ser Tyr Pro Ile Leu Glu Glu Arg Gly Asp Trp
 60 65 70
 gtg caa atc cag ctg aac ggc ggg caa aaa ggc tgg gtc gta tcc tgg 773

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Val	Gln	Ile	Gln	Leu	Asn	Gly	Gly	Gln	Lys	Gly	Trp	Val	Val	Ser	Trp	
75							80					85				
ctg	atc	aag	aaa	aag	agc	caa	gtc	tcc	agc	gga	tct	gat	tcc	gca	tcg	821
Leu	Ile	Lys	Lys	Lys	Ser	Gln	Val	Ser	Ser	Gly	Ser	Asp	Ser	Ala	Ser	
90						95					100					
gga	aaa	gtc	aca	tct	tcc	gaa	gca	aac	ttg	aga	atc	aga	aaa	ggc	ccc	869
Gly	Lys	Val	Thr	Ser	Ser	Glu	Ala	Asn	Leu	Arg	Ile	Arg	Lys	Gly	Pro	
105					110					115					120	
ggc	act	tca	tat	gaa	gtc	caa	ggc	gta	ttc	cct	gaa	gga	gaa	cag	gct	917
Gly	Thr	Ser	Tyr	Glu	Val	Gln	Gly	Val	Phe	Pro	Glu	Gly	Glu	Gln	Ala	
				125					130					135		
gac	ctg	cta	aag	acc	gac	gga	aaa	tgg	ata	aag	att	tcc	tat	cag	aac	965
Asp	Leu	Leu	Lys	Thr	Asp	Gly	Lys	Trp	Ile	Lys	Ile	Ser	Tyr	Gln	Asn	
			140					145					150			
atc	aca	ggc	tgg	gtc	tat	tca	gat	tat	gtc	aat	caa	ggt	tca	ggc	gcg	1013
Ile	Thr	Gly	Trp	Val	Tyr	Ser	Asp	Tyr	Val	Asn	Gln	Gly	Ser	Gly	Ala	
		155					160					165				
aaa	cag	tct	caa	tcg	tct	tca	tca	cat	gct	tca	tca	tca	aaa	tcg	gga	1061
Lys	Gln	Ser	Gln	Ser	Ser	Ser	Ser	His	Ala	Ser	Ser	Ser	Lys	Ser	Gly	
	170					175					180					
acg	gtc	ggc	gta	tcc	acc	tta	aat	gtc	agg	agc	aca	gct	tcc	cat	caa	1109
Thr	Val	Gly	Val	Ser	Thr	Leu	Asn	Val	Arg	Ser	Thr	Ala	Ser	His	Gln	
185					190				195						200	
ggc	cgg	att	att	gcc	acg	ctc	caa	cgg	aat	gca	agt	gtg	acg	att	tta	1157
Gly	Arg	Ile	Ile	Ala	Thr	Leu	Gln	Arg	Asn	Ala	Ser	Val	Thr	Ile	Leu	
				205					210					215		
aac	gaa	cag	cac	ggc	tgg	tat	gaa	atc	gaa	ttt	aat	gga	caa	aaa	ggc	1205
Asn	Glu	Gln	His	Gly	Trp	Tyr	Glu	Ile	Glu	Phe	Asn	Gly	Gln	Lys	Gly	
			220					225					230			
tgg	gcc	gca	agc	cac	tat	att	ctc	gaa	gga	aac	aaa	cag	aac	agc	gga	1253
Trp	Ala	Ala	Ser	His	Tyr	Ile	Leu	Glu	Gly	Asn	Lys	Gln	Asn	Ser	Gly	
		235					240						245			
acc	tcc	gga	aca	agc	agc	agc	tcc	gaa	gca	aaa	cgg	cag	ggc	acc	atc	1301
Thr	Ser	Gly	Thr	Ser	Ser	Ser	Ser	Glu	Ala	Lys	Arg	Gln	Gly	Thr	Ile	
	250					255					260					
gtg	tat	gaa	agc	aca	aat	gtt	aga	agc	ggg	gcc	tcg	aca	tcc	tca	gcg	1349
Val	Tyr	Glu	Ser	Thr	Asn	Val	Arg	Ser	Gly	Ala	Ser	Thr	Ser	Ser	Ala	
265					270				275						280	
atc	gtc	aaa	cgc	acg	gga	aaa	ggc	gag	tct	tac	ccg	atc	gtc	tct	aca	1397
Ile	Val	Lys	Arg	Thr	Gly	Lys	Gly	Glu	Ser	Tyr	Pro	Ile	Val	Ser	Thr	
				285					290					295		
aaa	gga	gac	tgg	tat	gaa	atc	aaa	ctg	tca	aac	ggc	gat	tcc	gct	tat	1445
Lys	Gly	Asp	Trp	Tyr	Glu	Ile	Lys	Leu	Ser	Asn	Gly	Asp	Ser	Ala	Tyr	
			300					305					310			
gtc	gca	agc	tgg	gtc	gtt	cag	act	gtt	gac	cag	gca	ggc	tca	gcc	gga	1493
Val	Ala	Ser	Trp	Val	Val	Gln	Thr	Val	Asp	Gln	Ala	Gly	Ser	Ala	Gly	
		315					320					325				
gat	tcg	aaa	agc	gca	gca	ccg	cct	ttg	gca	aag	cgg	tca	agc	tcg	gga	1541
Asp	Ser	Lys	Ser	Ala	Ala	Pro	Pro	Leu	Ala	Lys	Arg	Ser	Ser	Ser	Gly	
	330					335					340					
ggc	aca	atc	aaa	aat	aaa	acg	gtt	gtc	atc	gat	gcc	gga	cat	gga	gga	1589

10294.000.ST25.txt

Gly Thr Ile Lys Asn Lys Thr Val Val Ile Asp Ala Gly His Gly Gly
 345 350 355 360
 cat gac agc ggg aca atc gga acg cgg ggg acg ctc gaa aaa cgg ctg 1637
 His Asp Ser Gly Thr Ile Gly Thr Arg Gly Thr Leu Glu Lys Arg Leu
 365 370 375
 acc atc aaa acg gca acg ctt ctt gcc gcg aaa ctc aga gcc gat ggc 1685
 Thr Ile Lys Thr Ala Thr Leu Leu Ala Ala Lys Leu Arg Ala Asp Gly
 380 385 390
 gtc aac gtc tat atg acg cgg aat gac gat tct ttc gtc agc ctt cag 1733
 Val Asn Val Tyr Met Thr Arg Asn Asp Asp Ser Phe Val Ser Leu Gln
 395 400 405
 tcg cgg gtc gcg acc tct cat tac cga aac gcc gac gct ttt atc agc 1781
 Ser Arg Val Ala Thr Ser His Tyr Arg Asn Ala Asp Ala Phe Ile Ser
 410 415 420
 att cat tat gat agc ttt cca aat gcg tcc gtc agg gga aat acg gcc 1829
 Ile His Tyr Asp Ser Phe Pro Asn Ala Ser Val Arg Gly Asn Thr Ala
 425 430 435 440
 tat tac tac agc ccg tcc aaa gac cgg aag ctc gca gca gac gtg cag 1877
 Tyr Tyr Tyr Ser Pro Ser Lys Asp Arg Lys Leu Ala Ala Asp Val Gln
 445 450 455
 tcc gag atc gaa agg cac tcg cct ctg cca agc cgc ggc gta cta ttc 1925
 Ser Glu Ile Glu Arg His Ser Pro Leu Pro Ser Arg Gly Val Leu Phe
 460 465 470
 ggg gac tac ttc gta tta aga gaa aat aaa cag ccc gcc gca ttg ttt 1973
 Gly Asp Tyr Phe Val Leu Arg Glu Asn Lys Gln Pro Ala Ala Leu Phe
 475 480 485
 gaa ctc ggc tac ttg agc cat cct caa gaa gaa gcg gta gtc agc acg 2021
 Glu Leu Gly Tyr Leu Ser His Pro Gln Glu Glu Ala Val Val Ser Thr
 490 495 500
 aac gct tac aga gaa aga gtg aca gac ggc atc aga agc ggt cta gaa 2069
 Asn Ala Tyr Arg Glu Arg Val Thr Asp Gly Ile Arg Ser Gly Leu Glu
 505 510 515 520
 aac tat ttt gac taatttaaaa agctcccaat cgggagcttt ttatgctttc 2121
 Asn Tyr Phe Asp
 gaatccataa taaacgtgac gggacccgaa tttgtcagct tgacatccat catttctcca 2181
 aatcttcccg tttcgacagt gacgcctttt gcgcgaagca tgctgttcca ctcttcgtac 2241
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 gacaggttca tcttttcgcc ttcattctca aaaattcgca gattgacaag cttctccgcc 2421
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<210> 102

<211> 524

<212> PRT

<213> Bacillus licheniformis

<400> 102

Asn Met Lys Lys Arg Ala Val Leu Ile Leu Ser Met Met Leu Ala Ala
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Gln Ala Ala Phe Tyr Thr Ser Ser Asn Thr Ala Ser Ala Ala Ile Gly
 20 25 30

Glu Ala Val Ile Ala Thr Asp Glu Ile Asn Val Arg Ser Gly Pro Gly
 35 40 45

Leu Ser His Glu Ile Val Ser Val Val Ser Arg Asn Glu Ser Tyr Pro
 50 55 60

Ile Leu Glu Glu Arg Gly Asp Trp Val Gln Ile Gln Leu Asn Gly Gly
 65 70 75 80

Gln Lys Gly Trp Val Val Ser Trp Leu Ile Lys Lys Lys Ser Gln Val
 85 90 95

Ser Ser Gly Ser Asp Ser Ala Ser Gly Lys Val Thr Ser Ser Glu Ala
 100 105 110

Asn Leu Arg Ile Arg Lys Gly Pro Gly Thr Ser Tyr Glu Val Gln Gly
 115 120 125

Val Phe Pro Glu Gly Glu Gln Ala Asp Leu Leu Lys Thr Asp Gly Lys
 130 135 140

Trp Ile Lys Ile Ser Tyr Gln Asn Ile Thr Gly Trp Val Tyr Ser Asp
 145 150 155 160

Tyr Val Asn Gln Gly Ser Gly Ala Lys Gln Ser Gln Ser Ser Ser Ser
 165 170 175

His Ala Ser Ser Ser Lys Ser Gly Thr Val Gly Val Ser Thr Leu Asn
 180 185 190

Val Arg Ser Thr Ala Ser His Gln Gly Arg Ile Ile Ala Thr Leu Gln
 195 200 205

Arg Asn Ala Ser Val Thr Ile Leu Asn Glu Gln His Gly Trp Tyr Glu
 210 215 220

Ile Glu Phe Asn Gly Gln Lys Gly Trp Ala Ala Ser His Tyr Ile Leu
 225 230 235 240

10294.000.ST25.txt

Glu Gly Asn Lys Gln Asn Ser Gly Thr Ser Gly Thr Ser Ser Ser Ser
245 250 255

Glu Ala Lys Arg Gln Gly Thr Ile Val Tyr Glu Ser Thr Asn Val Arg
260 265 270

Ser Gly Ala Ser Thr Ser Ser Ala Ile Val Lys Arg Thr Gly Lys Gly
275 280 285

Glu Ser Tyr Pro Ile Val Ser Thr Lys Gly Asp Trp Tyr Glu Ile Lys
290 295 300

Leu Ser Asn Gly Asp Ser Ala Tyr Val Ala Ser Trp Val Val Gln Thr
305 310 315 320

Val Asp Gln Ala Gly Ser Ala Gly Asp Ser Lys Ser Ala Ala Pro Pro
325 330 335

Leu Ala Lys Arg Ser Ser Ser Gly Gly Thr Ile Lys Asn Lys Thr Val
340 345 350

Val Ile Asp Ala Gly His Gly Gly His Asp Ser Gly Thr Ile Gly Thr
355 360 365

Arg Gly Thr Leu Glu Lys Arg Leu Thr Ile Lys Thr Ala Thr Leu Leu
370 375 380

Ala Ala Lys Leu Arg Ala Asp Gly Val Asn Val Tyr Met Thr Arg Asn
385 390 395 400

Asp Asp Ser Phe Val Ser Leu Gln Ser Arg Val Ala Thr Ser His Tyr
405 410 415

Arg Asn Ala Asp Ala Phe Ile Ser Ile His Tyr Asp Ser Phe Pro Asn
420 425 430

Ala Ser Val Arg Gly Asn Thr Ala Tyr Tyr Tyr Ser Pro Ser Lys Asp
435 440 445

Arg Lys Leu Ala Ala Asp Val Gln Ser Glu Ile Glu Arg His Ser Pro
450 455 460

Leu Pro Ser Arg Gly Val Leu Phe Gly Asp Tyr Phe Val Leu Arg Glu
465 470 475 480

Asn Lys Gln Pro Ala Ala Leu Phe Glu Leu Gly Tyr Leu Ser His Pro
485 490 495

Gln Glu Glu Ala Val Val Ser Thr Asn Ala Tyr Arg Glu Arg Val Thr
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10294.000.ST25.txt
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 515 520

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 gatgcctata tgaaaggcga taaggcgctg ttctcaaaaa gagaagaagt cattgaaaag 240
 aatattaagg cgcttgaaga cgaaacagtc agcgctgatt ccaaagttga caaacagcgg 300
 tttttgtatg agcttgaaac aagcaagctt gatatgaagg ctgctgaaga aattgagccg 360
 ttgatcgtgc ttgataacca ggctgccggc atgtcgccta agaaaagagc ggtgctgggc 420
 gtactgatcg gtttagcgct gtcatttttc atcattgtca ttccggaagt tttcagagaa 480
 cgttaaattt ttaattgggg atgtggatca ggacc atg acg agg caa aaa cct 533
 Met Thr Arg Gln Lys Pro
 1 5
 tta atc tct gtc att acg cct tcc tat aac gcg gag gaa ttt atc gaa 581
 Leu Ile Ser Val Ile Thr Pro Ser Tyr Asn Ala Glu Glu Phe Ile Glu
 10 15 20
 aaa acc att aag tcc gtc tta aat cag acg ttt tcc gac tgg gaa atg 629
 Lys Thr Ile Lys Ser Val Leu Asn Gln Thr Phe Ser Asp Trp Glu Met
 25 30 35
 atc att gcc gat gat tgc tca aca gat ggg aca aga gac att ttg aag 677
 Ile Ile Ala Asp Asp Cys Ser Thr Asp Gly Thr Arg Asp Ile Leu Lys
 40 45 50
 cgc tat gaa gaa gat gat gag cgg atc cat gcc att ttt ctg aaa gag 725
 Arg Tyr Glu Glu Asp Asp Glu Arg Ile His Ala Ile Phe Leu Lys Glu
 55 60 65 70
 aat caa ggt gct gca gcg gcg cga aat gcg gcg ctc agc aaa gcc gaa 773
 Asn Gln Gly Ala Ala Ala Arg Asn Ala Ala Leu Ser Lys Ala Glu
 75 80 85
 ggg cgc tat gtc gcc ttt ttg gac agc gat gat gtt tgg aaa gca gaa 821
 Gly Arg Tyr Val Ala Phe Leu Asp Ser Asp Asp Val Trp Lys Ala Glu
 90 95 100

10294.000.ST25.txt

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tca ttt acg gca tac gag ctg atc agc caa gac ggc gaa ccg ctt cat Ser Phe Thr Ala Tyr Glu Leu Ile Ser Gln Asp Gly Glu Pro Leu His 120 125 130	917
aaa acc att cat gca ccc gta agc ctt aca tat gat gat gta tta aaa Lys Thr Ile His Ala Pro Val Ser Leu Thr Tyr Asp Asp Val Leu Lys 135 140 145 150	965
aat acg atc atc ggc tgc ttg acg gtg atg att gac aga gaa caa acg Asn Thr Ile Ile Gly Cys Leu Thr Val Met Ile Asp Arg Glu Gln Thr 155 160 165	1013
ggt gat atc cgg atg ccg aat att aga acc cgc cag gat ttg gcg aca Gly Asp Ile Arg Met Pro Asn Ile Arg Thr Arg Gln Asp Leu Ala Thr 170 175 180	1061
tgg ctg tcc gta tta aag cgg ggg ttc aag gca tat gga ctg aac gaa Trp Leu Ser Val Leu Lys Arg Gly Phe Lys Ala Tyr Gly Leu Asn Glu 185 190 195	1109
ccc ctc gcg gaa tac cgc atc gtt gaa aca tcg atc tcc aga aac aag Pro Leu Ala Glu Tyr Arg Ile Val Glu Thr Ser Ile Ser Arg Asn Lys 200 205 210	1157
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ctt cac ttg atg aaa gcg aca tgg tgc ttt ttc cat tac gct aag aac Leu His Leu Met Lys Ala Thr Trp Cys Phe Phe His Tyr Ala Lys Asn 235 240 245	1253
gca gta atg aaa aga tta taacggcatt gacagaaaag gtgattgaaa Ala Val Met Lys Arg Leu 250	1301
gtgaaagcag atcaattcat acacgtcata gtagcgacag gtgaatgggg gcaggatcag	1361
ctaagataca gaaggcaccg ccttgctgag tttttagcag gccgcaagga gacgaaggaa	1421
gtcatttggg tttgtccgtc tgaaaatcct tcccgtgaga cttttacatt gcttgacaac	1481
ggaatcaagc aatttgcagt caaagatttt ttgaaaaaga aaatattcag gtttgcccgc	1541
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gttcagggag aaaagggtgtg cttatggtac accttccccg gctttccgct gctgtcgtcg	1661
ctttatcaat gggatcaggt catctatgac tgcagcgacc tgtgggcggc cccgatcagc	1721
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<211> 252

<212> PRT

<213> Bacillus licheniformis

<400> 104

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 Phe Ser Asp Trp Glu Met Ile Ile Ala Asp Asp Cys Ser Thr Asp Gly
 35 40 45
 Thr Arg Asp Ile Leu Lys Arg Tyr Glu Glu Asp Asp Glu Arg Ile His
 50 55 60
 Ala Ile Phe Leu Lys Glu Asn Gln Gly Ala Ala Ala Arg Asn Ala
 65 70 75 80
 Ala Leu Ser Lys Ala Glu Gly Arg Tyr Val Ala Phe Leu Asp Ser Asp
 85 90 95
 Asp Val Trp Lys Ala Glu Lys Leu Asp Lys Gln Leu Ala Phe Met Arg
 100 105 110
 Lys His Gln His Ala Phe Ser Phe Thr Ala Tyr Glu Leu Ile Ser Gln
 115 120 125
 Asp Gly Glu Pro Leu His Lys Thr Ile His Ala Pro Val Ser Leu Thr
 130 135 140
 Tyr Asp Asp Val Leu Lys Asn Thr Ile Ile Gly Cys Leu Thr Val Met
 145 150 155 160
 Ile Asp Arg Glu Gln Thr Gly Asp Ile Arg Met Pro Asn Ile Arg Thr
 165 170 175
 Arg Gln Asp Leu Ala Thr Trp Leu Ser Val Leu Lys Arg Gly Phe Lys
 180 185 190
 Ala Tyr Gly Leu Asn Glu Pro Leu Ala Glu Tyr Arg Ile Val Glu Thr
 195 200 205
 Ser Ile Ser Arg Asn Lys Trp Lys Ala Ala Arg Lys Thr Trp Tyr Val
 210 215 220
 Tyr Arg Glu Ile Glu Arg Leu His Leu Met Lys Ala Thr Trp Cys Phe
 225 230 235 240
 Phe His Tyr Ala Lys Asn Ala Val Met Lys Arg Leu
 245 250

<210> 105

<211> 1309

<212> DNA

<213> *Bacillus licheniformis*

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<222> (485)..(808)

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aatcaacacc gaaaatgaag gaactcccgg tcagatgaaa aaaatcgtcg acacagtgaa      180
gaaaaaggac gtcccggcct tattcgtgga gacaagcggt gacccgcgga gcatggaaaag      240
cctttcagcc gaaacgggcg tgccgattaa agcaaaagtc ttcaccgatt cgatcgaaaa      300
gcccggtgga agcgggagat tcctattata agatgatgaa agaaaacctt gaccggatcc      360
atcaaggcct cgccgaataa ccaatgaact gctgtacagg atgtacagca gtttttttct      420
tatgtttttc cgatttttaa gcagggtaca acgaagggaa aacgaggaaa aaggagtgtg      480
tttc gtg aaa tct gga tat gag gaa tgc atc aaa gcc tgc cga gaa tgt      529
    Val Lys Ser Gly Tyr Glu Glu Cys Ile Lys Ala Cys Arg Glu Cys
      1          5          10          15

ctt gaa gcc tgc aac cac tgc ttt gac aaa tgt ctg atg gaa gaa gag      577
Leu Glu Ala Cys Asn His Cys Phe Asp Lys Cys Leu Met Glu Glu Glu
      20          25          30

gct ggg atg atg gcc gaa tgc atc cgt ctt gac cgg gaa tgc gcg gag      625
Ala Gly Met Met Ala Glu Cys Ile Arg Leu Asp Arg Glu Cys Ala Glu
      35          40          45

atg tgc ggt tac gca att caa gcc atg acg cgc aac agc ccg tat gcc      673
Met Cys Gly Tyr Ala Ile Gln Ala Met Thr Arg Asn Ser Pro Tyr Ala
      50          55          60

gaa gat att tgc cag ctt tgc gca aag gtt tgc gaa gct tgc ggc aat      721
Glu Asp Ile Cys Gln Leu Cys Ala Lys Val Cys Glu Ala Cys Gly Asn
      65          70          75

gaa tgc agc cag cac aag cat gac cac tgc caa ttt tgc gct gaa agc      769
Glu Cys Ser Gln His Lys His Asp His Cys Gln Phe Cys Ala Glu Ser
      80          85          90          95

tgc ttt gca tgc gcg gaa gcg tgc aga aaa atg gct tct taacttgaaa      818
Cys Phe Ala Cys Ala Glu Ala Cys Arg Lys Met Ala Ser
      100          105

catccggccc tcgagccgga ttttttatg taggaaatgt ttattttttc tccttcccc      878
tttctaaact gatacaatat gactataaaa gggggtttta tcatgaaaga cagcgtgttt      938
caaatgactt ctgacacata tcaatctctc agcgattcag aacggcattt gctcgagtac      998

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10294.000.ST25.txt

atttatcagc acttagacgt catcgccact ttatcgattg taaaattaag cgaggatgca 1058
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tcttttaagt atgcattaaa agaaaaacac cacctcggac acgctccgct gatggatgat 1178
atcgacagcc aaattaaaca ggccgtgcta aagaatgaaa gagaagttct ggatacgatt 1238
aagatgcttg atatcggggt gatcgaagat gccattcaaa aaatcagcaa tgccgaaaaa 1298
gtttacatct t 1309

<210> 106

<211> 108

<212> PRT

<213> Bacillus licheniformis

<400> 106

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20 25 30

Gly Met Met Ala Glu Cys Ile Arg Leu Asp Arg Glu Cys Ala Glu Met
35 40 45

Cys Gly Tyr Ala Ile Gln Ala Met Thr Arg Asn Ser Pro Tyr Ala Glu
50 55 60

Asp Ile Cys Gln Leu Cys Ala Lys Val Cys Glu Ala Cys Gly Asn Glu
65 70 75 80

Cys Ser Gln His Lys His Asp His Cys Gln Phe Cys Ala Glu Ser Cys
85 90 95

Phe Ala Cys Ala Glu Ala Cys Arg Lys Met Ala Ser
100 105

<210> 107

<211> 1561

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (284)..(1060)

<223>

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tccaaacagg aagtcaaagt ccgcgaagtt atgattgaag gcatcctttc gatcttggaa      180
ggccaggctc caaaagtcac tgaacaaaag cttttgatgt acgtttctcc aagcgaacgc      240
tccagcatcg tcatcccaga tggagacaaa ggggacagca gca atg gct aga aaa      295
                                     Met Ala Arg Lys
                                     1

aag aag cac aaa aaa gac cat gaa gaa cac gtg gat gag tct tgg ctc      343
Lys Lys His Lys Lys Asp His Glu Glu His Val Asp Glu Ser Trp Leu
5                               10                               15                               20

atc cca tat gca gac ttg ctg aca ctg ctt ttg gcc ctg ttc atc gta      391
Ile Pro Tyr Ala Asp Leu Leu Thr Leu Leu Ala Leu Phe Ile Val
                               25                               30                               35

ctg ttt gcc atg agc tcg atc gac gcc aag aag ttc gat atg ctg tca      439
Leu Phe Ala Met Ser Ser Ile Asp Ala Lys Lys Phe Asp Met Leu Ser
                               40                               45                               50

aaa tca ttt aat gcc gta ttt acc ggc gga aca gga atg atg gat tat      487
Lys Ser Phe Asn Ala Val Phe Thr Gly Gly Thr Gly Met Met Asp Tyr
55                               60                               65

tcc agc ttc acc gag ccg aaa acg agc aca acc gaa gat gga aaa agc      535
Ser Ser Phe Thr Glu Pro Lys Thr Ser Thr Thr Glu Asp Gly Lys Ser
70                               75                               80

cct gac cag gca aaa gat ctc tcc gaa gct caa aaa gaa aaa gac aag      583
Pro Asp Gln Ala Lys Asp Leu Ser Glu Ala Gln Lys Glu Lys Asp Lys
85                               90                               95                               100

cag tcg ctg aaa aaa att cag gag cag gtc aac cgg ttt att aaa gag      631
Gln Ser Leu Lys Lys Ile Gln Glu Gln Val Asn Arg Phe Ile Lys Glu
105                               110                               115

aag aat ctt caa aaa cag gtc aat acg aag ctg aca gac gag ggc ctc      679
Lys Asn Leu Gln Lys Gln Val Asn Thr Lys Leu Thr Asp Glu Gly Leu
120                               125                               130

ctc ctt tcc atc gag gat aat atc ttt ttc gat tcc gga aaa gcg gag      727
Leu Leu Ser Ile Glu Asp Asn Ile Phe Phe Asp Ser Gly Lys Ala Glu
135                               140                               145

atc cgc cag cag gac att ccg ctg gcc aag gaa gta tcc gac ctt ctc      775
Ile Arg Gln Gln Asp Ile Pro Leu Ala Lys Glu Val Ser Asp Leu Leu
150                               155                               160

gta ttg aac ccg ccc cgc aat atc gta atc agc ggg cat acg gac aat      823
Val Leu Asn Pro Pro Arg Asn Ile Val Ile Ser Gly His Thr Asp Asn
165                               170                               175                               180

gtg ccg att cga aat tct caa ttt aaa tca aat tgg cat tta agc gtg      871
Val Pro Ile Arg Asn Ser Gln Phe Lys Ser Asn Trp His Leu Ser Val
185                               190                               195

atg ccg gct gtc aat ttc atg ggg ctt tta atc gaa aat cca aag ctt      919

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10294.000.ST25.txt

Met Arg Ala Val Asn Phe Met Gly Leu Leu Ile Glu Asn Pro Lys Leu
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gac gcc aag atc ttc agc gcg aaa ggc tac ggg gaa ttt aaa ccg atc 967
 Asp Ala Lys Ile Phe Ser Ala Lys Gly Tyr Gly Glu Phe Lys Pro Ile
 215 220 225

gct tca aat gac acc gaa gaa gga aga aga aaa aac aga cgc gtt gaa 1015
 Ala Ser Asn Asp Thr Glu Glu Gly Arg Arg Lys Asn Arg Arg Val Glu
 230 235 240

atc ctt atc ctg ccg atc ggc cag gaa aat ctg aat aaa aaa gaa 1060
 Ile Leu Ile Leu Pro Ile Gly Gln Glu Asn Leu Asn Lys Lys Glu
 245 250 255

taaggaagct gtcttttggc agcttcctta ctctttgccc ttataaatat ttcttgcat 1120
 cagtccgact ttttcagca tttcgatgca ggcttctttc tcctcatcgc ttaatacgct 1180
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 aaactcgggt ggattcagac catgatgatg aatatgttta ttcatatgat cattaatgga 1480
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 catatcactc atctccaaag a 1561

<210> 108

<211> 259

<212> PRT

<213> Bacillus licheniformis

<400> 108

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 20 25 30

Leu Phe Ile Val Leu Phe Ala Met Ser Ser Ile Asp Ala Lys Lys Phe
 35 40 45

Asp Met Leu Ser Lys Ser Phe Asn Ala Val Phe Thr Gly Gly Thr Gly
 50 55 60

Met Met Asp Tyr Ser Ser Phe Thr Glu Pro Lys Thr Ser Thr Thr Glu
 65 70 75 80

Asp Gly Lys Ser Pro Asp Gln Ala Lys Asp Leu Ser Glu Ala Gln Lys
 85 90 95

10294.000.ST25.txt

Glu Lys Asp Lys Gln Ser Leu Lys Lys Ile Gln Glu Gln Val Asn Arg
100 105 110
Phe Ile Lys Glu Lys Asn Leu Gln Lys Gln Val Asn Thr Lys Leu Thr
115 120 125
Asp Glu Gly Leu Leu Leu Ser Ile Glu Asp Asn Ile Phe Phe Asp Ser
130 135 140
Gly Lys Ala Glu Ile Arg Gln Gln Asp Ile Pro Leu Ala Lys Glu Val
145 150 155 160
Ser Asp Leu Leu Val Leu Asn Pro Pro Arg Asn Ile Val Ile Ser Gly
165 170 175
His Thr Asp Asn Val Pro Ile Arg Asn Ser Gln Phe Lys Ser Asn Trp
180 185 190
His Leu Ser Val Met Arg Ala Val Asn Phe Met Gly Leu Leu Ile Glu
195 200 205
Asn Pro Lys Leu Asp Ala Lys Ile Phe Ser Ala Lys Gly Tyr Gly Glu
210 215 220
Phe Lys Pro Ile Ala Ser Asn Asp Thr Glu Glu Gly Arg Arg Lys Asn
225 230 235 240
Arg Arg Val Glu Ile Leu Ile Leu Pro Ile Gly Gln Glu Asn Leu Asn
245 250 255

Lys Lys Glu

<210> 109
<211> 1735
<212> DNA
<213> Bacillus licheniformis

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<222> (501)..(1232)
<223>

<400> 109
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Page 209

10294.000.ST25.txt

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cccgaactca gcaagacaag agcaaaacaa ccccttggtc agcctgcctg tgccaaccga	180
cgagctcgtc aagaatacag acgcagtcacat cgtcactcat tcggacccgg atttctctcc	240
tataaactag aagcctcatg ttgaaaaagt attttatatt gaaaaagaat tctatctggg	300
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cagaatttta tataaaatca aactttatca gtaaaaaaac tgtaacgaaa ttcgcatcaa	420
tctgtcatag cgggtgacatt ttgctgtgtt acgattttcc ctgttagttt caaaagggct	480
aacaagggag gatttaactt atg aag aag aca atc atg tcc ttg gct gca gcc	533
Met Lys Lys Thr Ile Met Ser Leu Ala Ala Ala	
1 5 10	
gcg gct atg tcg gcg act gca ttc gga gcg act gcc tca gca aaa gaa	581
Ala Ala Met Ser Ala Thr Ala Phe Gly Ala Thr Ala Ser Ala Lys Glu	
15 20 25	
atc gaa gtt caa aaa gga gac acg ctc tgg ggg att tct caa aac tac	629
Ile Glu Val Gln Lys Gly Asp Thr Leu Trp Gly Ile Ser Gln Asn Tyr	
30 35 40	
gga atg aac ctc aag gac tta aaa aaa tgg aat cag ctt tca tca gat	677
Gly Met Asn Leu Lys Asp Leu Lys Lys Trp Asn Gln Leu Ser Ser Asp	
45 50 55	
ctg att ttt cca ggt caa aag ctg aac att tct tct caa gaa gaa aaa	725
Leu Ile Phe Pro Gly Gln Lys Leu Asn Ile Ser Ser Gln Glu Glu Lys	
60 65 70 75	
tct gaa gaa aag cag tac acc gtt cag cca ggg gac acg ctc tca aaa	773
Ser Glu Glu Lys Gln Tyr Thr Val Gln Pro Gly Asp Thr Leu Ser Lys	
80 85 90	
atc gca aaa gag ttc ggt gtg act gta agc gat ctt caa aaa cgg aac	821
Ile Ala Lys Glu Phe Gly Val Thr Val Ser Asp Leu Gln Lys Arg Asn	
95 100 105	
aac ctg aag tca gac ttg att att gca ggg caa acg att gca ata aac	869
Asn Leu Lys Ser Asp Leu Ile Ile Ala Gly Gln Thr Ile Ala Ile Asn	
110 115 120	
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Gly Glu Ala Ala Ala Ala Ala Pro Val Lys Gln Glu Ser Ala Pro	
125 130 135	
aaa caa aat gat cag cct gtc aac gta caa aag gaa atc aca gtg acc	965
Lys Gln Asn Asp Gln Pro Val Asn Val Gln Lys Glu Ile Thr Val Thr	
140 145 150 155	
gca act gcg tat acg gca aat gac ggg ggc att tca ggc atc aca aaa	1013
Ala Thr Ala Tyr Thr Ala Asn Asp Gly Gly Ile Ser Gly Ile Thr Lys	
160 165 170	
acg gga gtc gac ctg aat gcg aac cgc aat gcg aaa gtc atc gcg gtt	1061
Thr Gly Val Asp Leu Asn Ala Asn Arg Asn Ala Lys Val Ile Ala Val	
175 180 185	
gat cca agc gtg att ccg ctc ggc acg aaa gta tat gtg gaa ggc tat	1109
Asp Pro Ser Val Ile Pro Leu Gly Thr Lys Val Tyr Val Glu Gly Tyr	
190 195 200	
ggc gaa gcg acg gct gaa gac acc ggc ggc gcc att aaa ggc cat aaa	1157

10294.000.ST25.txt

Gly	Glu	Ala	Thr	Ala	Glu	Asp	Thr	Gly	Gly	Ala	Ile	Lys	Gly	His	Lys	
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Ile	Asp	Val	Phe	Ile	Pro	Asp	Lys	Lys	Asp	Ala	Phe	Asn	Trp	Gly	Val	
220					225				230					235		
aaa	acc	gta	aag	gtt	aaa	att	tta	aac	tgatataaaa	aatgcaggag						1252
Lys	Thr	Val	Lys	Val	Lys	Ile	Leu	Asn								
				240												
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cgt	tgc	ttt	ttac	aaaaaac	cgaaatcgca	agagcggcgg	ctgcaaaggc	gatggctacg								1372
aaata	aaacca	tatga	acgcc	ttctgtcatg	ccttgcatgt	gcagctcctg	acggctgcct									1432
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ggacc	gattg	cccctgaaac	ttgattaact	gtattcatta	tcgccgaacc	atgcgggtaa										1552
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ccgagt	gtaa	agccggcgta	gagcatcatt	ccgaccgcca	tcggcgtatc	gcttgaaata										1672
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aag																1735

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<211> 244

<212> PRT

<213> Bacillus licheniformis

<400> 110

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Thr	Ala	Phe	Gly	Ala	Thr	Ala	Ser	Ala	Lys	Glu	Ile	Glu	Val	Gln	Lys
			20				25						30		

Gly	Asp	Thr	Leu	Trp	Gly	Ile	Ser	Gln	Asn	Tyr	Gly	Met	Asn	Leu	Lys
		35				40					45				

Asp	Leu	Lys	Lys	Trp	Asn	Gln	Leu	Ser	Ser	Asp	Leu	Ile	Phe	Pro	Gly
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Gln	Lys	Leu	Asn	Ile	Ser	Ser	Gln	Glu	Glu	Lys	Ser	Glu	Glu	Lys	Gln
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Tyr	Thr	Val	Gln	Pro	Gly	Asp	Thr	Leu	Ser	Lys	Ile	Ala	Lys	Glu	Phe
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Gly	Val	Thr	Val	Ser	Asp	Leu	Gln	Lys	Arg	Asn	Asn	Leu	Lys	Ser	Asp
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10294.000.ST25.txt

Leu Ile Ile Ala Gly Gln Thr Ile Ala Ile Asn Gly Glu Ala Ala Ala
115 120 125

Ala Ala Ala Pro Val Lys Gln Glu Ser Ala Pro Lys Gln Asn Asp Gln
130 135 140

Pro Val Asn Val Gln Lys Glu Ile Thr Val Thr Ala Thr Ala Tyr Thr
145 150 155 160

Ala Asn Asp Gly Gly Ile Ser Gly Ile Thr Lys Thr Gly Val Asp Leu
165 170 175

Asn Ala Asn Arg Asn Ala Lys Val Ile Ala Val Asp Pro Ser Val Ile
180 185 190

Pro Leu Gly Thr Lys Val Tyr Val Glu Gly Tyr Gly Glu Ala Thr Ala
195 200 205

Glu Asp Thr Gly Gly Ala Ile Lys Gly His Lys Ile Asp Val Phe Ile
210 215 220

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225 230 235 240

Lys Ile Leu Asn

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<211> 1731

<212> DNA

<213> Bacillus licheniformis

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<222> (507)..(1274)

<223>

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cgaccataca aaataagagc attctttttt aagcaacgtc tttggtttct tcggccgctt 240
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10294.000.ST25.txt.

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		Met	Ile	Ser	Trp	Leu	Ser	Leu	Ala	Ser						
		1				5										
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Ala	Arg	Glu	Asn	Arg	Val	Leu	Lys	Ala	Glu	Phe	Ser	Leu	Gly	Arg	Leu	
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Lys	Lys	Glu	Leu	Asn	Val	Phe	Phe	Ile	Ser	Asp	Ile	His	Arg	Arg	Thr	
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Val	Ser	Glu	Asp	Ile	Ile	Cys	Glu	Val	Lys	Glu	Arg	Gly	Val	Gln	Leu	
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Ile	Glu	Glu	Asn	Ile	Lys	Arg	Leu	Ser	Ser	Leu	Gly	Lys	Thr	Tyr	Phe	
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His	Asp	His	Gln	Gly	Gln	Thr	Val	Asn	Ile	Cys	Gly	Val	Asp	Asp	Ile	
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Arg	Leu	Glu	Leu	Asp	Asp	Tyr	Pro	Ala	Ala	Leu	Gly	Gly	Val	Gln	Pro	
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Gly	Phe	Pro	Thr	Val	Leu	Val	Ser	His	Asn	Pro	Glu	Ile	His	His	Gln	
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ata	cag	gag	gcg	gac	ggt	att	gac	ctg	ata	ttg	agc	ggt	cat	acc	cac	1109
Ile	Gln	Glu	Ala	Asp	Gly</											

Thr Ser Lys Leu Pro Ala Gly Ile Leu Gly Val Pro Ala Ile Ala Met
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 Ala Tyr Val Gly Glu Glu Phe 250 255
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 35 40 45
 Phe Ile Ser Asp Ile His Arg Arg Thr Val Ser Glu Asp Ile Ile Cys
 50 55 60
 Glu Val Lys Glu Arg Gly Val Gln Leu Val Ile Ile Gly Gly Asp Leu
 65 70 75 80
 Ala Glu Gly Gly Val Pro Tyr Thr Arg Ile Glu Glu Asn Ile Lys Arg
 85 90 95
 Leu Ser Ser Leu Gly Lys Thr Tyr Phe Val Trp Gly Asn Asn Asp Tyr
 100 105 110
 Glu Val Asp Gln Glu Arg Leu Leu Glu Ile Phe Lys Thr Tyr Gly Val
 115 120 125

Thr Pro Leu Arg Asn Ala Ser Val Leu His Asp His Gln Gly Gln Thr
 130 135 140

Val Asn Ile Cys Gly Val Asp Asp Ile Arg Leu Glu Leu Asp Asp Tyr
 145 150 155 160

Pro Ala Ala Leu Gly Gly Val Gln Pro Gly Phe Pro Thr Val Leu Val
 165 170 175

Ser His Asn Pro Glu Ile His His Gln Ile Gln Glu Ala Asp Gly Ile
 180 185 190

Asp Leu Ile Leu Ser Gly His Thr His Gly Gly Gln Ile Arg Phe Gly
 195 200 205

Arg Phe Gly Leu Cys Glu Ile Gly Gly Thr Gly Thr Val Phe Lys Ala
 210 215 220

Pro Tyr Leu Ile Ser Asn Gly Tyr Gly Thr Ser Lys Leu Pro Ala Gly
 225 230 235 240

Ile Leu Gly Val Pro Ala Ile Ala Met Ala Tyr Val Gly Glu Glu Phe
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<210> 113

<211> 1722

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<213> Bacillus licheniformis

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<222> (540)..(788)

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 gtttttttca ttttcttctt ctgcggttaa actggagggc gtatcgaatc aatgtgtgaa 360
 tttttcgtca ggacagccgt tcaaacagtc aacaagatgc tgaacaaaca gaataaatta 420
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 Val Leu Phe Phe Ala Leu Tyr Ser Ala Ala Ala Leu Pro Ser Ala His
 20 25 30
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 Ala Ala Asn Glu Lys Lys Pro Thr Val Thr Ser His Thr Tyr Lys Asn
 35 40 45
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 Ile Lys Ala Leu Lys Tyr Pro Gln Val Ser Asn Val Ser Pro Lys Ser
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 Leu Gln Asn Lys Ile Asn Lys Asp Phe Lys His Tyr Ile Glu Gln Ser
 65 70 75 80
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 Tyr Lys Asp
 aacggattat caaacgtcct ttgaagtga ataccggacc ggccaaaagc tgagcatcct 888
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 <211> 83
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 <213> Bacillus licheniformis

10294.000.ST25.txt

<400> 114

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 Val Leu Phe Phe Ala Leu Tyr Ser Ala Ala Ala Leu Pro Ser Ala His
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 35 40 45
 Ile Lys Ala Leu Lys Tyr Pro Gln Val Ser Asn Val Ser Pro Lys Ser
 50 55 60
 Leu Gln Asn Lys Ile Asn Lys Asp Phe Lys His Tyr Ile Glu Gln Ser
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Tyr Lys Asp

<210> 115

<211> 1705

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (507)..(1202)

<223>

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 tcaatttata aaacaggagg atgtat atg aaa aag aaa atc agc ata ttg atc 533
 Met Lys Lys Lys Ile Ser Ile Leu Ile
 1 5
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10294.000.ST25.txt

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tac Tyr	tcc Ser	ggc Gly 45	ggc Gly	gca Ala	ttg Leu	ctt Leu	ttg Leu	gac Asp 50	cct Pro	att Ile	ccg Pro	tcc Ser	aat Asn 55	atg Met	aag Lys	677
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<211> 232

<212> PRT

<213> Bacillus licheniformis

<400> 116

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 35 40 45

Leu Asp Pro Ile Pro Ser Asn Met Lys Ile Thr Ala Leu Asn Pro Thr
 50 55 60

Asp Met Asn Tyr Arg Gly Val Lys Ala Ala Leu Ala Gly Ala Tyr Leu
 65 70 75 80

Arg Val Glu Gly Pro Lys Gly Lys Thr Thr Val Tyr Val Thr Asp Leu
 85 90 95

Tyr Pro Glu Gly Ala Pro Gly Ala Leu Asp Leu Ser Pro Asn Ala Phe
 100 105 110

Arg Glu Ile Gly Asp Met Lys Asp Gly Lys Ile Asp Ile Lys Trp Arg
 115 120 125

Ile Val Lys Ala Pro Ile Thr Gly Asn Phe Thr Tyr Arg Ile Lys Glu
 130 135 140

Gly Ser Ser Gln Trp Trp Ala Ala Ile Gln Val Arg Asn His Lys Tyr
 145 150 155 160

Pro Val Met Lys Met Glu Tyr Tyr Lys Asp Gly Lys Trp Ile Asn Met
 165 170 175

Glu Lys Thr Asp Tyr Asn His Phe Val Ser Thr Asn Leu Gly Thr Ser
 180 185 190

Pro Leu Lys Val Arg Ile Thr Asp Ile Arg Gly Lys Val Val Lys Asp
 195 200 205

Thr Ile Lys Lys Leu Pro Glu Asn Gly Thr Ser Ser Ala Tyr Thr Val
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Pro Gly Lys Val Gln Phe Pro Asp
225 230

<210> 117

<211> 1687

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1184)

<223>

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cag gag gta aca gtt gcc gaa gat gcg ccc aac gtt gcg att atg ctt 629
Gln Glu Val Thr Val Ala Glu Asp Ala Pro Asn Val Ala Ile Met Leu
30 35 40

gat gca agc ggc agc atg gct aaa aag atc ggc ggg gtc tca aaa tac 677
Asp Ala Ser Gly Ser Met Ala Lys Lys Ile Gly Gly Val Ser Lys Tyr
45 50 55

gag ctt gcc aaa aat gaa gcg ttc agc ttt ggt tcc aag ctt gaa aat 725
Glu Leu Ala Lys Asn Glu Ala Phe Ser Phe Gly Ser Lys Leu Glu Asn
60 65 70 75

gca aac gtg ctc atg aga gtt ttc ggt tca gag gga aac aat aaa aat 773

10294.000.ST25.txt

Ala Asn Val Leu Met Arg Val Phe Gly Ser Glu Gly Asn Asn Lys Asn
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Ser Gly Lys Val Gln Ser Cys Asn Ala Ile Arg Gly Val Tyr Gly Phe
95 100 105

caa acg tat gac gag caa agc ttc cgc aat tcc tta aac ggc atc gga 869
Gln Thr Tyr Asp Glu Gln Ser Phe Arg Asn Ser Leu Asn Gly Ile Gly
110 115 120

ccg acc gga tgg aca ccg atc gca aac gcg ctg caa gat gca aaa aac 917
Pro Thr Gly Trp Thr Pro Ile Ala Asn Ala Leu Gln Asp Ala Lys Asn
125 130 135

gcg ctt gac cag ctg gac aac aac ggg aaa aac gtc gtc tat ctg ctg 965
Ala Leu Asp Gln Leu Asp Asn Asn Gly Lys Asn Val Val Tyr Leu Leu
140 145 150 155

aca gac ggt gag gaa aca tgc gga ggc aat ccg gta aaa gtc gca aca 1013
Thr Asp Gly Glu Glu Thr Cys Gly Gly Asn Pro Val Lys Val Ala Thr
160 165 170

gaa ctg cgc aaa tcc aat gcg gtt gtc aac gtg atc ggc ttt gat tat 1061
Glu Leu Arg Lys Ser Asn Ala Val Val Asn Val Ile Gly Phe Asp Tyr
175 180 185

gaa gga gac ttc cac gga caa ttg acc agt atc gca gca gct ggc ggc 1109
Glu Gly Asp Phe His Gly Gln Leu Thr Ser Ile Ala Ala Ala Gly Gly
190 195 200

ggt gaa tat ttc cag gca aaa act aaa aat gac atc aaa aga att ttt 1157
Gly Glu Tyr Phe Gln Ala Lys Thr Lys Asn Asp Ile Lys Arg Ile Phe
205 210 215

act cag gaa gca att gag ctt tct aaa taaactggaa aaaagctgtg 1204
Thr Gln Glu Ala Ile Glu Leu Ser Lys
220 225

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atctcatgcg gaagatcggg ccgaaaaaac aaatgcggaa aggaaagtga gaaagttgaa 1564

aaagagggtt gctctgttga caacgttcac catgcttttg tcattggcgc cggcagcagc 1624

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gct 1687

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<211> 228

<212> PRT

<213> Bacillus licheniformis

<400> 118

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 35 40 45
 Met Ala Lys Lys Ile Gly Gly Val Ser Lys Tyr Glu Leu Ala Lys Asn
 50 55 60
 Glu Ala Phe Ser Phe Gly Ser Lys Leu Glu Asn Ala Asn Val Leu Met
 65 70 75 80
 Arg Val Phe Gly Ser Glu Gly Asn Asn Lys Asn Ser Gly Lys Val Gln
 85 90 95
 Ser Cys Asn Ala Ile Arg Gly Val Tyr Gly Phe Gln Thr Tyr Asp Glu
 100 105 110
 Gln Ser Phe Arg Asn Ser Leu Asn Gly Ile Gly Pro Thr Gly Trp Thr
 115 120 125
 Pro Ile Ala Asn Ala Leu Gln Asp Ala Lys Asn Ala Leu Asp Gln Leu
 130 135 140
 Asp Asn Asn Gly Lys Asn Val Val Tyr Leu Leu Thr Asp Gly Glu Glu
 145 150 155 160
 Thr Cys Gly Gly Asn Pro Val Lys Val Ala Thr Glu Leu Arg Lys Ser
 165 170 175
 Asn Ala Val Val Asn Val Ile Gly Phe Asp Tyr Glu Gly Asp Phe His
 180 185 190
 Gly Gln Leu Thr Ser Ile Ala Ala Ala Gly Gly Gly Glu Tyr Phe Gln
 195 200 205
 Ala Lys Thr Lys Asn Asp Ile Lys Arg Ile Phe Thr Gln Glu Ala Ile
 210 215 220
 Glu Leu Ser Lys
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<210> 119

<211> 1428

<212> DNA

<213> Bacillus licheniformis .10294.000.ST25.txt

<220>

<221> CDS

<222> (501)..(944)

<223>

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cttggcgagt atcatccgta tttttgggca tcaaagcttc atttttatat tacgtctggt 180
ccgtttttaca attttcctta tacgttcggc tacttggttt cgcttggcat ttacgcgcaa 240
gcgctgaaag aggggtgcggc atttgaagaa aaatatattg ctctcttaaa agatacagcc 300
tccatgtctg ttgaagaact ggccatgaag catctcggcg ccgatctgac gaagcgggat 360
ttctgggaag cggccattca gccggctgtc cgagatgcag aagcattttt agcgatgaca 420
taaagtcttc cgcttagatt gaatgagttt ccgcaaagtg gacatagcta aggataatgt 480
gcatagagga gatgaacggg atg aat caa ttt cgg atg gcc gtt atc gct ctc 533
Met Asn Gln Phe Arg Met Ala Val Ile Ala Leu
1 5 10
gtc ctg atc ctg atg acc ggc tgc ggc tcc ata gcg gaa gaa cat gcg 581
Val Leu Ile Leu Met Thr Gly Cys Gly Ser Ile Ala Glu Glu His Ala
15 20 25
gaa ggc aag gag gcc gtt ccc gat aac gcc cct gtt tca gat gtg aaa 629
Glu Gly Lys Glu Ala Val Pro Asp Asn Ala Pro Val Ser Asp Val Lys
30 35 40
agc gtg cct tac gct gca ttt gca ttg gaa gtg aac tat ggc cat gga 677
Ser Val Pro Tyr Ala Ala Phe Ala Leu Glu Val Asn Tyr Gly His Gly
45 50 55
aag cac aat acg ttt gaa gcc gta tac gac aaa cag gag cgg gaa gaa 725
Lys His Asn Thr Phe Glu Ala Val Tyr Asp Lys Gln Glu Arg Glu Glu
60 65 70 75
gca tcg att aaa gac tat ctg aac gga gcg gac cgc gaa ggg gag gaa 773
Ala Ser Ile Lys Asp Tyr Leu Asn Gly Ala Asp Arg Glu Gly Glu Glu
80 85 90
gct tta aac gaa atg aaa atg gtt tta agc gag ctt tcg atc gcc aaa 821
Ala Leu Asn Glu Met Lys Met Val Leu Ser Glu Leu Ser Ile Ala Lys
95 100 105
tcc gat cca gag cag gac gtg atc agc aat gtg ctc gag gcc ttc aat 869
Ser Asp Pro Glu Gln Asp Val Ile Ser Asn Val Leu Glu Ala Phe Asn
110 115 120
ctt gac gaa caa tat gac cgg ttt cag ctg cgg gtg aaa tgg cct gat 917
Leu Asp Glu Gln Tyr Asp Arg Phe Gln Leu Arg Val Lys Trp Pro Asp
125 130 135
ggc acg tcc aga atc tat aac gga aaa taaacaaaag agcatttcca 964

Gly Thr Ser Arg Ile Tyr Asn Gly Lys
140 145

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cgtttccggt ttttacagcg ttcaattttt tccacagcgg atcgcttgtc caatcgtttt 1144
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ttcccgggaa agaatcttta tagtaaattcc ttgattggcc ggccataaat ctgattaccg 1384
acacccgttt ctttttctgg tcgccgagct tgtcgttaa ttcg 1428

<210> 120

<211> 148

<212> PRT

<213> Bacillus licheniformis

<400> 120

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20 25 30

Val Pro Asp Asn Ala Pro Val Ser Asp Val Lys Ser Val Pro Tyr Ala
35 40 45

Ala Phe Ala Leu Glu Val Asn Tyr Gly His Gly Lys His Asn Thr Phe
50 55 60

Glu Ala Val Tyr Asp Lys Gln Glu Arg Glu Glu Ala Ser Ile Lys Asp
65 70 75 80

Tyr Leu Asn Gly Ala Asp Arg Glu Gly Glu Glu Ala Leu Asn Glu Met
85 90 95

Lys Met Val Leu Ser Glu Leu Ser Ile Ala Lys Ser Asp Pro Glu Gln
100 105 110

Asp Val Ile Ser Asn Val Leu Glu Ala Phe Asn Leu Asp Glu Gln Tyr
115 120 125

Asp Arg Phe Gln Leu Arg Val Lys Trp Pro Asp Gly Thr Ser Arg Ile
130 135 140

Tyr Asn Gly Lys
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<210> 121

<211> 1589

<212> DNA

<213> Bacillus licheniformis

<220>

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<222> (501)..(1109)

<223>

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gcgagggtta cggacacgga agcgggtttg ctttaattgt tgttctgttc attctcttaa 180
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tgttgactcc atcatgaaag gctctttttt aaaaaagagc ctttttttaa tgcaatacag 360
ataccgaacc tctcctgctg ctgaatgtta atagaaaatt aatgtttttt tcaaaaagag 420
acatgatttt cattctatta atgctattat ttttccatcc tattaataaa taggaaaatt 480
aagagagggga gtgttggtat atg ttt aaa act aag ttc aag aaa aca att ggg 533
Met Phe Lys Thr Lys Phe Lys Lys Thr Ile Gly
1 5 10
att gga ctc gtt gcc gct gcc tgt ttg att tcc gcg tcg gcg gca agc 581
Ile Gly Leu Val Ala Ala Ala Cys Leu Ile Ser Ala Ser Ala Ala Ser
15 20 25
gct gcg tcg caa aat gaa agc gat gtt aaa gtg aaa ctg gac gat cag 629
Ala Ala Ser Gln Asn Glu Ser Asp Val Lys Val Lys Leu Asp Asp Gln
30 35 40
cag cgg aat caa tat acg gtc aaa tct ttc cac tac tta acc gtt gac 677
Gln Arg Asn Gln Tyr Thr Val Lys Ser Phe His Tyr Leu Thr Val Asp
45 50 55
gga aaa aat gtg gat tcg tcg gct caa gcc aac gcc aaa tcc gtc aga 725
Gly Lys Asn Val Asp Ser Ser Ala Gln Ala Asn Ala Lys Ser Val Arg
60 65 70 75
gat gtc aaa gta acc atg gtt ctg ccc aag cag aat aag aac ggc gat 773
Asp Val Lys Val Thr Met Val Leu Pro Lys Gln Asn Lys Asn Gly Asp
80 85 90
ttg ctt gcg tat gga ttt acg agc aag gtt act tta gaa gcc ttt atc 821
Leu Leu Ala Tyr Gly Phe Thr Ser Lys Val Thr Leu Glu Ala Phe Ile
95 100 105

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gcg aaa gac aag cag agg ctt gag aag caa ttc aaa cct tct gcc agc Ala Lys Asp Lys Gln Arg Leu Glu Lys Gln Phe Lys Pro Ser Ala Ser 110 115 120	869
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tat att tac tgg aga gac gga ttt aaa aac ttg cca tcc agc tgg aat Tyr Ile Tyr Trp Arg Asp Gly Phe Lys Asn Leu Pro Ser Ser Trp Asn 140 145 150 155	965
gac aga att tca tgc tta agt acg gcg tct cct tca tca agc tat tca Asp Arg Ile Ser Ser Leu Ser Thr Ala Ser Pro Ser Ser Ser Tyr Ser 160 165 170	1013
acg acg ctg tgg gag cat act tca act caa gga tac ggc aaa ggc gtt Thr Thr Leu Trp Glu His Thr Ser Thr Gln Gly Tyr Gly Lys Gly Val 175 180 185	1061
ttg ttt aga cat tcc gat tgg tac ggc act aat tgc agc tgc gca ccc Leu Phe Arg His Ser Asp Trp Tyr Gly Thr Asn Ser Ser Ser Ala Pro 190 195 200	1109
tgataaatta cttttttttg cgatgccggt gttgttgatc ggttcatcat gaccgataca	1169
gctgatgaca tggatggtag tcatattccc cgggagccgt ttaacatcag attctgccgc	1229
ctgctttaaa aatgccttga gatctgtatc cgctttttgt tcgttcaggt gcaggagttt	1289
aacatacata tcatagatca gctgttttgt cagttcagac atagtcaatg gacagtcctt	1349
tcttttttatt ttccggttaa caaaatatatt taatagttta tttcaggatt tgtcaatatt	1409
atgataaggt gaaatcagat aacaaatgtg ttttgtttat catgaaacaa caccaaaaag	1469
gagaatcgct gatgaatatt gaaggaatag agatggaagt tcgctgcaca ggcgatgtat	1529
gttcagatgc ccttgaattt ttgagacgcc ataaccacga aaaaacagcc gaacattcga	1589

<210> 122

<211> 203

<212> PRT

<213> Bacillus licheniformis

<400> 122

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Glu Ser Asp Val Lys Val Lys Leu Asp Asp Gln Gln Arg Asn Gln Tyr 35 40 45
Thr Val Lys Ser Phe His Tyr Leu Thr Val Asp Gly Lys Asn Val Asp 50 55 60

10294.000.ST25.txt

ser ser Ala Gln Ala Asn Ala Lys Ser Val Arg Asp Val Lys Val Thr
65 70 75 80

Met Val Leu Pro Lys Gln Asn Lys Asn Gly Asp Leu Leu Ala Tyr Gly
85 90 95

Phe Thr Ser Lys Val Thr Leu Glu Ala Phe Ile Ala Lys Asp Lys Gln
100 105 110

Arg Leu Glu Lys Gln Phe Lys Pro Ser Ala Ser Gly Pro Cys Cys Thr
115 120 125

Asp Phe Tyr Glu Tyr Lys Asn Lys Gly Gly Gln Tyr Ile Tyr Trp Arg
130 135 140

Asp Gly Phe Lys Asn Leu Pro Ser Ser Trp Asn Asp Arg Ile Ser Ser
145 150 155 160

Leu Ser Thr Ala Ser Pro Ser Ser Ser Tyr Ser Thr Thr Leu Trp Glu
165 170 175

His Thr Ser Thr Gln Gly Tyr Gly Lys Gly Val Leu Phe Arg His Ser
180 185 190

Asp Trp Tyr Gly Thr Asn Ser Ser Ser Ala Pro
195 200

<210> 123

<211> 1522

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1019)

<223>

<400> 123

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aagacgaaaa ggcgcgtttc gggtttggaat acgtctgaaa gcagcgctct tgaagtcggt	180
tcaaacaaag cgcggcataa tccgtttaag gcattcatga taaagaatgt ccagacatga	240
tcggcgagtg caaaaccggc gaacacgaac gtccagccga aaatcgagac gagcatgatg	300

10294.000.ST25.txt

gttttccggc cgaacctgtc tgataagtac ccgccataaa agcttgccgc aattccgatc 360
 agagagctcg ctgcaatgac agctcccgca aagccggaag aggcgccttt cacttggtgc 420
 aaataaattg ctaaaaaagg gatgactcat ggcgtgttcc tcatgcgctt taaggtaagg 480
 caaaaaagaa ggtgatattg atg tac agc cga agc aag ttc aaa atc ggt tta 533
 Met Tyr Ser Arg Ser Lys Phe Lys Ile Gly Leu
 1 5 10
 ttg ctt att gga agt ctg ctg gcc gcg ctc agc ttt cac ctg gag gcc 581
 Leu Leu Ile Gly Ser Leu Leu Ala Ala Leu Ser Phe His Leu Glu Ala
 15 20 25
 ttg gcc gaa aag ccg gct aaa gtt caa atc cag ctt gaa aag gtt tat 629
 Leu Ala Glu Lys Pro Ala Lys Val Gln Ile Gln Leu Glu Lys Val Tyr
 30 35 40
 ctg gac gga gac gtt gga att gag aat aaa gta gag gcc gct cgc aca 677
 Leu Asp Gly Asp Val Gly Ile Glu Asn Lys Val Glu Ala Ala Arg Thr
 45 50 55
 ctg gaa gac ttt aaa gct gct tat aaa ggg tgg cag ctc atc gat cag 725
 Leu Glu Asp Phe Lys Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln
 60 65 70 75
 aaa aag ggg ttt att ctg ttt cgc aaa cag gtg gac gac att tct ccc 773
 Lys Lys Gly Phe Ile Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro
 80 85 90
 ctc agc aaa aca aac ggt tat atc gga gtg act gaa gat ggc gtg att 821
 Leu Ser Lys Thr Asn Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile
 95 100 105
 tcg act ttt cac ggt cgc ccg ggc atc tta tca gaa ccc att caa tcg 869
 Ser Thr Phe His Gly Arg Pro Gly Ile Leu Ser Glu Pro Ile Gln Ser
 110 115 120
 ttt ttt cag att gat ata aag cgg ctg gaa agc cgg atg gcg gat gat 917
 Phe Phe Gln Ile Asp Ile Lys Arg Leu Glu Ser Arg Met Ala Asp Asp
 125 130 135
 ctg cgc aaa ggg ata cca tac cgc acg aaa aag gaa ttt gaa cat gtc 965
 Leu Arg Lys Gly Ile Pro Tyr Arg Thr Lys Lys Glu Phe Glu His Val
 140 145 150 155
 att gaa gcc gta aaa tca tcc gga agc caa cat cat gta gaa gat atg 1013
 Ile Glu Ala Val Lys Ser Ser Gly Ser Gln His His Val Glu Asp Met
 160 165 170
 aag aca tgacgctgtt atgtcttttt tcagctgcag acagaagctt ttttagcgaa 1069
 Lys Thr
 catatgttaa ctttttcatt ctagctttgc ctgttttggt ttacaatgaa gagcagtcaa 1129
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 gcgctgtacg gcttttcgac aaggggaagaa aaaatgctgt ttacgaaaat gctgaatgtt 1369
 acgggggatcg gcccaaaagg agcgttgcg atcctcgctt ccggcgatcc gggagcggtg 1429
 attgaagcga tcgagaatga ggacgaagca tttctcgta aatttcccg cgtaggcaaa 1489

aaaacggcaa ggcagatcat ccttgacctg aaa

1522

<210> 124

<211> 173

<212> PRT

<213> Bacillus licheniformis

<400> 124

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20 25 30Ala Lys Val Gln Ile Gln Leu Glu Lys Val Tyr Leu Asp Gly Asp Val
35 40 45Gly Ile Glu Asn Lys Val Glu Ala Ala Arg Thr Leu Glu Asp Phe Lys
50 55 60Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln Lys Lys Gly Phe Ile
65 70 75 80Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro Leu Ser Lys Thr Asn
85 90 95Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile Ser Thr Phe His Gly
100 105 110Arg Pro Gly Ile Leu Ser Glu Pro Ile Gln Ser Phe Phe Gln Ile Asp
115 120 125Ile Lys Arg Leu Glu Ser Arg Met Ala Asp Asp Leu Arg Lys Gly Ile
130 135 140Pro Tyr Arg Thr Lys Lys Glu Phe Glu His Val Ile Glu Ala Val Lys
145 150 155 160Ser Ser Gly Ser Gln His His Val Glu Asp Met Lys Thr
165 170

<210> 125

<211> 1492

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(989)

<223>

<400> 125

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ggcgtcgttt taccttaaaa tgttgtggcc gtatttttta ttccactttt ttgcgatgcc    180
ttttcaggcc tgtttaatcg gaatgggggt ggccaaagat gctttttatc ataacgtttg    240
ggccagtgtc ttatcgtttt tgatgatgta tgttctcggg tccatgcaga ctttgcagat    300
gacgggggac attcttgcga tgaataccgg tatgattttg ctgacggcgc tgcattatgt    360
gacgatttgc aaggagctgg gcgtcacgct ttttttgaca aacaaatccc gatctccgag    420
aattgaaagc cgctgatgga tcctcttcat agtttttagct tttgcgggga agctaataatt    480
aaaaaagaag gggagttccc atg cga aga atc agt ctc att tac ccg ctc atc    533
                        Met Arg Arg Ile Ser Leu Ile Tyr Pro Leu Ile
                        1           5           10

ctg ctg ttt ttt acc ggg tta ttc gta ttt cag ccg cag gca tct gca      581
Leu Leu Phe Phe Thr Gly Leu Phe Val Phe Gln Pro Gln Ala Ser Ala
                        15           20           25

aaa caa gct tgc ccg gca gtc atg cag atg aac acg gtc gaa ggt cag      629
Lys Gln Ala Ser Pro Ala Val Met Gln Met Asn Thr Val Glu Gly Gln
                        30           35           40

cgc gtc gtc att ccc gcc gaa ggc cag aag acg atc gtt cat ttt tgg      677
Arg Val Val Ile Pro Ala Gln Gly Gln Lys Thr Ile Val His Phe Trp
                        45           50           55

acg acc tgg tgc ccg cca tgc cgt gaa gag ctt ccg cga ttc caa tcc      725
Thr Thr Trp Cys Pro Pro Cys Arg Glu Glu Leu Pro Arg Phe Gln Ser
                        60           65           70           75

tac tat gaa agc aag caa tcc ggc gtc aag ctc gtg acc gtt aat tta      773
Tyr Tyr Glu Ser Lys Gln Ser Gly Val Lys Leu Val Thr Val Asn Leu
                        80           85           90

ctg aat gcc gaa aag aac gaa cag aag gta aaa cag ttt att aaa gca      821
Leu Asn Ala Glu Lys Asn Glu Gln Lys Val Lys Gln Phe Ile Lys Ala
                        95           100           105

aac aag ctg aca ttt ccg atc gtt ttt gac aaa aag ggt gag atg atg      869
Asn Lys Leu Thr Phe Pro Ile Val Phe Asp Lys Lys Gly Glu Met Met
                        110           115           120

aaa gca tat aaa gtc atg aca att cct acg act ttt ttc ttt aat gaa      917
Lys Ala Tyr Lys Val Met Thr Ile Pro Thr Thr Phe Phe Phe Asn Glu
                        125           130           135

aaa gga gag ctg gag aaa acg ttt gtc ggc ccc att act gta gaa cag      965
Lys Gly Glu Leu Glu Lys Thr Phe Val Gly Pro Ile Thr Val Glu Gln
                        140           145           150           155

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atg aag gaa tgg gca ggg aaa agc tgagccggga gttcagcttt ttttaaaatg 1019
Met Lys Glu Trp Ala Gly Lys Ser
160

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tatataaata aaataacttaa tgtttatgct gccgatgagg cggcaatttg ttttttaaga 1199
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gcaatgaaac attgtccgtt gttctgttta ttttagcttt ttgtatcggc ggcttttgcta 1439
aagcgaaaga aggtatacaa gaaacgctgt cggaaaaaac gctgaatgtt gaa 1492

<210> 126

<211> 163

<212> PRT

<213> Bacillus licheniformis

<400> 126

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Ala Val Met Gln Met Asn Thr Val Glu Gly Gln Arg Val Val Ile Pro
35 40 45

) Ala Glu Gly Gln Lys Thr Ile Val His Phe Trp Thr Thr Trp Cys Pro
50 55 60

Pro Cys Arg Glu Glu Leu Pro Arg Phe Gln Ser Tyr Tyr Glu Ser Lys
65 70 75 80

Gln Ser Gly Val Lys Leu Val Thr Val Asn Leu Leu Asn Ala Glu Lys
85 90 95

Asn Glu Gln Lys Val Lys Gln Phe Ile Lys Ala Asn Lys Leu Thr Phe
100 105 110

Pro Ile Val Phe Asp Lys Lys Gly Glu Met Met Lys Ala Tyr Lys Val
115 120 125

Met Thr Ile Pro Thr Thr Phe Phe Phe Asn Glu Lys Gly Glu Leu Glu
130 135 140

Gly Lys Ser

<211> 1477

<213> Bacillus licheniformis

<221> CDS

<223>

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ctg atc ggt ttt tat atg gcg gaa tac cca aaa tgg aac ggg caa agc 629
Leu Ile Gly Phe Tyr Met Ala Glu Tyr Pro Lys Trp Asn Gly Gln Ser
30 35 40

ctg ttc ggc gga gag ctc tac tgg aca ggc gac cgc ggc aag ctg gac 725
Leu Phe Gly Gly Glu Leu Tyr Trp Thr Gly Asp Arg Gly Lys Leu Asp 75

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10294.000.ST25.txt

Asp Thr Tyr Leu Glu Lys Leu Val Val Lys Phe Gly Asp Glu Ile Val
80 85 90

ttg aac gcc caa atc gaa acg ccg gtg aaa gat tac gcg gga ggc aaa 821
Leu Asn Ala Gln Ile Glu Thr Pro Val Lys Asp Tyr Ala Gly Gly Lys
95 100 105

ttc ccc ggc gga ggg tca aaa gaa caa tcc gtt tct ttt ttg gaa ggg 869
Phe Pro Gly Gly Gly Ser Lys Glu Gln Ser Val Ser Phe Leu Glu Gly
110 115 120

ctt gaa gaa gct gaa atc gcc ggc cgc gag gtg acg gtt caa ttg gat 917
Leu Glu Glu Ala Glu Ile Ala Gly Arg Glu Val Thr Val Gln Leu Asp
125 130 135

tgg aga gag ggc aaa caa gcg tcc cat aca gga ttt acg ctt gat aaa 965
Trp Arg Glu Gly Lys Gln Ala Ser His Thr Gly Phe Thr Leu Asp Lys
140 145 150 155

agc tca tgg taaaaggcgg aatatcgatt atattccgcc tacctcaatt 1014
Ser Ser Trp

ttgcttcgca tcgtcagctc ttctgcggc cccaaatccc gaaatccggt cacactcttc 1074
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gaggcaggaa gagtaaacag gcacttttct ttatcccctg attcgtttaa aggatagcgg 1434
aaagatgtgt gatacccaa tccgatcggc atcggtatctt gac 1477

<210> 128

<211> 158

<212> PRT

<213> Bacillus licheniformis

<400> 128

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20 25 30

Met Ala Glu Tyr Pro Lys Trp Asn Gly Gln Ser Ala Asp Gly Asn Trp
35 40 45

Glu Ala Val Ile Lys Lys Ile Asp Gly Arg Ala Leu Phe Gly Gly Glu
50 55 60

Leu Tyr Trp Thr Gly Asp Arg Gly Lys Leu Asp Asp Thr Tyr Leu Glu
65 70 75 80

Lys Leu Val Val Lys Phe Gly Asp Glu Ile Val Leu Asn Ala Gln Ile
85 90 95

Glu Thr Pro Val Lys Asp Tyr Ala Gly Gly Lys Phe Pro Gly Gly Gly
100 105 110

Ser Lys Glu Gln Ser Val Ser Phe Leu Glu Gly Leu Glu Glu Ala Glu
115 120 125

Ile Ala Gly Arg Glu Val Thr Val Gln Leu Asp Trp Arg Glu Gly Lys
130 135 140

Gln Ala Ser His Thr Gly Phe Thr Leu Asp Lys Ser Ser Trp
145 150 155

<210> 129

<211> 1219

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (812)..(1114)

<223>

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tcaccaggaa acctaccgct tcaccaggaa accaaccact tcaccaggaa accaacactc 240
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cgtattctca ataaactctc taatggttga atcagaatag attttcgtct gcattcatca 420
cttatcgta tctgttcgag tgtactgcgt tccctaactg acgtggaacc acgtgctgaa 480
cagtggacta tctctcgctc tctccataac ctggcttatc cttcgcgcg ggtcttaaaa 540
catgctctcc tataagcagc tttgggtaat gtctgcttat tccatcacc tcgcaaccgt 600
gttttttgca attatggacg cgctggaggc ggtggttcca agtcagttcc tcctgaactg 660
gtttgtgaac ttatcatgc tgtttctcgc cattaagaa acgccggctt cttaaagcagc 720

ac

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Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly Val Thr Tyr Lys Phe
85 90 95

Pro Val Tyr Pro Asp
100

<210> 131
<211> 1381
<212> DNA
<213> Bacillus licheniformis

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cgccatccct aaggcgccat ctatcagctg cgcaaataat cctatcaaga caaacacaat 180
cagctttttc atgttggcct cccacttcaa ttggttttatt tttattgtta aatataatct 240
atactatgcc tacctgtaaa gtgcgagttt tataaaatat aaattttttg tatttttcat 300
cgacaccagc aaaaaagagc atatgcatgc aaaatgagcg cctatcccc ggtcttttgt 360
cttaatgaaa gacagtttat ggatgctgct tgcaaaaaat gcatcgtgca gaaaaggcgt 420
cggggagtaa cgcctcattc gtttcattgg caatgatgat ataatcccc atgtaatgac 480
ttcaaaagga ggctcaagcc atg aaa ttc agc aaa atc ggt gcc tta ctg ctc 533
Met Lys Phe Ser Lys Ile Gly Ala Leu Leu Leu
1 5 10
act ttg gcg tgt ttg ctt ttg cct ttt tct tcg gcg act gca gca ggt 581
Thr Leu Ala Cys Leu Leu Leu Pro Phe Ser Ser Ala Thr Ala Ala Gly
15 20 25
gcc ggt gta tgg gat aat atc ggc aca tac ggc atg acg tcg caa act 629
Ala Gly Val Trp Asp Asn Ile Gly Thr Tyr Gly Met Thr Ser Gln Thr
30 35 40
ccg atc atc aaa tca agc gga ggg gaa ttt tat ttt cac aac aac agc 677
Pro Ile Ile Lys Ser Ser Gly Gly Glu Phe Tyr Phe His Asn Asn Ser
45 50 55
ttt tac ggc ttt aca ttt acg ctg tat gaa gtt gac ggg gcg gga agc 725
Phe Tyr Gly Phe Thr Phe Thr Leu Tyr Glu Val Asp Gly Ala Gly Ser
60 65 70 75
acg cct gaa atc gca aga aaa aat ttc tac gtc gga ccg aaa agc aac 773
Thr Pro Glu Ile Ala Arg Lys Asn Phe Tyr Val Gly Pro Lys Ser Asn
80 85 90

10294.000.ST25.txt

agt ccg gcg atc gat gtc agc agt ttt gca gat ggt gcg aat aaa caa 821
 Ser Pro Ala Ile Asp Val Ser Ser Phe Ala Asp Gly Ala Asn Lys Gln
 95 100 105

gca gaa ctc gtc ctg ttt aaa ggg aat gat aca tat atc acc gtt act 869
 Ala Glu Leu Val Leu Phe Lys Gly Asn Asp Thr Tyr Ile Thr Val Thr
 110 115 120

tgt tat gat tgaatgtccc ataaacagca agccccccgt ttacagccgg 918
 Cys Tyr Asp
 125

cgggtttttt tgatcaagtt ccttccttat acctataggc acaaaaaagt gcctatatga 978

cttaaaagtg cgtacttccg ttttggtgtc ttctgttcca taatcataat tgatgttttg 1038

tttgacattg ttctgtttat aatgaaaaga aaacggaggg atcaatgatg aacttggtatt 1098

tacggggaaa aagagcgttg gtgaccggat cgacgtccgg aatcggcaaa gcgattgccg 1158

cttcacttgc gaaagaaggt gcgtctgtca tcattaacgg acgccggcaa gaaaagggtca 1218

accaaacaat agacgaattg aaaggccaat ttcccagggc tgttcttcaa gcggcccctt 1278

atgaccttgg cactgaaaaa ggggtgtcaa gcctatttagc agcattcccc gatgttgata 1338

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<210> 132

<211> 126

<212> PRT

<213> Bacillus licheniformis

<400> 132

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 20 25 30

Asn Ile Gly Thr Tyr Gly Met Thr Ser Gln Thr Pro Ile Ile Lys Ser
 35 40 45

Ser Gly Gly Glu Phe Tyr Phe His Asn Asn Ser Phe Tyr Gly Phe Thr
 50 55 60

Phe Thr Leu Tyr Glu Val Asp Gly Ala Gly Ser Thr Pro Glu Ile Ala
 65 70 75 80

Arg Lys Asn Phe Tyr Val Gly Pro Lys Ser Asn Ser Pro Ala Ile Asp
 85 90 95

Val Ser Ser Phe Ala Asp Gly Ala Asn Lys Gln Ala Glu Leu Val Leu
 100 105 110

Phe Lys Gly Asn Asp Thr Tyr Ile Thr Val Thr Cys Tyr Asp
 115 120 125

<210> 133

<211> 1581

<212> DNA

<213> Bacillus licheniformis

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<221> CDS

<222> (601)..(978)

<223>

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 ggtagataag atttgaattt ggtgacttgc ttttgttctt cttctttcat tttctgacta 240
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 ggtcactaac cgaatgcagt aaaggacact gtggtgcttg ccagccatta gggatttgag 360
 gaggtgatca aaatgctagg tgacagtatt tcgtcgaagt ggacaagtcg tgaccaaagt 420
 acctcggatc gagggtttgt catggaggaa aaaattgatg tctggtgaca aagaggagtc 480
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 ggtgacaaac taacttatag agtaaattta ttagtcgaat gaaagaggag gaatgaaata 600
 atg aaa aat cat ttg tat gag aaa aaa aag agg aaa cct ttg act cgg 648
 Met Lys Asn His Leu Tyr Glu Lys Lys Lys Arg Lys Pro Leu Thr Arg
 1 5 10 15
 aca att aaa gcg acg ctc gcc gtg ttg aca atg tcc atc gct ttg gtg 696
 Thr Ile Lys Ala Thr Leu Ala Val Leu Thr Met Ser Ile Ala Leu Val
 20 25 30
 gga ggc gct acg gtg cct tca ttt gca tgg gtg aat ccg ggt tat cac 744
 Gly Gly Ala Thr Val Pro Ser Phe Ala Trp Val Asn Pro Gly Tyr His
 35 40 45
 tac cag tac cca tcg gaa ggt ggt aca tgg agg tat gga ttc gta aac 792
 Tyr Gln Tyr Pro Ser Glu Gly Gly Thr Trp Arg Tyr Gly Phe Val Asn
 50 55 60
 gcc ggg ctc cgt tca gag tac aac cac ccg aca aag gtc cac ggc tcg 840
 Ala Gly Leu Arg Ser Glu Tyr Asn His Pro Thr Lys Val His Gly Ser
 65 70 75 80
 aca gtg caa aag ctc atc gat gga aaa gtg gat aaa acg aat aga agt 888
 Page 238

10294.000.ST25.txt

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Thr Val Gln Lys Leu Ile Asp Gly Lys Val Asp Lys Thr Asn Arg Ser
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att gat acg gct gcg ggc cgc tac tct aat gcc tat gtc gga gcc ata 936
Ile Asp Thr Ala Ala Gly Arg Tyr Ser Asn Ala Tyr Val Gly Ala Ile
      100      105      110
aac tca cct ggt ctt aag ggt cgt tac tac tat cgc acc aac 978
Asn Ser Pro Gly Leu Lys Gly Arg Tyr Tyr Tyr Arg Thr Asn
      115      120      125
taatcaaagg gaaaacgggt gctgtcaacg gggctagcat ggcaagaccc agaaaagttc 1038
tgaggagatcc cgctttgcat aagcgtatta tagtggatga cgcgggcttt gttgtttaca 1098
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tgctttcggg gtactgccaa agcatctcca caaaagatag tgcatactcg caggaaaaaa 1518
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tct 1581

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<210> 134

<211> 126

<212> PRT

<213> Bacillus licheniformis

<400> 134

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      20      25      30
Gly Gly Ala Thr Val Pro Ser Phe Ala Trp Val Asn Pro Gly Tyr His
      35      40      45
Tyr Gln Tyr Pro Ser Glu Gly Gly Thr Trp Arg Tyr Gly Phe Val Asn
      50      55      60
Ala Gly Leu Arg Ser Glu Tyr Asn His Pro Thr Lys Val His Gly Ser
      65      70      75      80
Thr Val Gln Lys Leu Ile Asp Gly Lys Val Asp Lys Thr Asn Arg Ser
      85      90      95

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Ile Asp Thr Ala Ala Gly Arg Tyr Ser Asn Ala Tyr Val Gly Ala Ile
 100 105 110

Asn Ser Pro Gly Leu Lys Gly Arg Tyr Tyr Tyr Arg Thr Asn
 115 120 125

<210> 135

<211> 1357

<212> DNA

<213> Bacillus licheniformis

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 ttgacgcaaa agagaagatt tgcttttcga cgtctctaatt attttcaaac agcaccgctt 180
 cagccgctga aagcgcagcc tctgagattt cccagctcag ccgaacgggt tcatgatccg 240
 gcgaagttat ttttaaaata tcgttacaaa acgaagaatc gcctcgaata ctatgttgaa 300
 aagggttttt cccgatgatt gtccttttca ccgcgcgccc tcccgtaag ccttgttatg 360
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 ttttattttt tgcattaact ctttttgaag caagcgtttt tatggtataa aaaagaagga 480
 gaaaattaga attgaagggtg atg aac gtg gaa att gct atc att gcg ctg ctc 533
 Met Asn Val Glu Ile Ala Ile Ile Ala Leu Leu
 1 5 10
 gtt gtc agt att gcg ctg att gca ttc tca tat ttt caa aga gaa ccg 581
 Val Val Ser Ile Ala Leu Ile Ala Phe Ser Tyr Phe Gln Arg Glu Pro
 15 20 25
 atc aag gaa gtt gaa cag gag ttg gaa acc ctt cag ctg tcc gcc atg 629
 Ile Lys Glu Val Glu Gln Glu Leu Glu Thr Leu Gln Leu Ser Ala Met
 30 35 40
 cag gaa atc tat aaa ctg aaa aag aag atg acc gtg ctt gag gaa gag 677
 Gln Glu Ile Tyr Lys Leu Lys Lys Lys Met Thr Val Leu Glu Glu Glu
 45 50 55
 ctc ctc gat tca aat gtg gtc gtc cgc aga ccg aat gcc gga atc agc 725
 Leu Leu Asp Ser Asn Val Val Val Arg Arg Pro Asn Ala Gly Ile Ser
 60 65 70 75
 cag cat att gcg aag cag att ctt tca aaa tat caa aac ggc atg tct 773
 Page 240

Gln His Ile Ala Lys Gln Ile Leu Ser Lys Tyr Gln Asn Gly Met Ser
80 85 90

gta gac gcc atc gca aaa gct gag cac gta tct gtc gaa gat gtc aaa 821
Val Asp Ala Ile Ala Lys Ala Glu His Val Ser Val Glu Asp Val Lys
95 100 105

gcg atc att aaa gac tat gag agg gtg ctt gta tgaccagaca gagtgtaaa 874
Ala Ile Ile Lys Asp Tyr Glu Arg Val Leu Val
110 115

gcatttgccc ggagaatgga ttgtggctac cgccgttctt gcaagcgcat tttatttgaa 934
cggataatac gacccgattt acctgtgcga tgcgaagatt ctccgtcagc atcagactgt 994
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cggtgcgttc ctggttcata aagtttcccc agcgtccgat cgcttgacca agcagaatgc 1294
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<211> 118

<212> PRT

<213> Bacillus licheniformis

<400> 136

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Leu Ile Ala Phe Ser Tyr Phe Gln Arg Glu Pro Ile Lys Glu Val Glu
20 25 30

Gln Glu Leu Glu Thr Leu Gln Leu Ser Ala Met Gln Glu Ile Tyr Lys
35 40 45

Leu Lys Lys Lys Met Thr Val Leu Glu Glu Glu Leu Leu Asp Ser Asn
50 55 60

Val Val Val Arg Arg Pro Asn Ala Gly Ile Ser Gln His Ile Ala Lys
65 70 75 80

Gln Ile Leu Ser Lys Tyr Gln Asn Gly Met Ser Val Asp Ala Ile Ala
85 90 95

Lys Ala Glu His Val Ser Val Glu Asp Val Lys Ala Ile Ile Lys Asp
100 105 110

Tyr Glu Arg Val Leu Val
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<210> 137

<211> 1297

<212> DNA

<213> Bacillus licheniformis

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<222> (501)..(794)

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ttcttaaacg ttgatatgac gcagttttta cgaagattta accgtcgaat tttcgacctg 180
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gtgctacgat ccgaagggtt taatacagta tttgaagggtc ctctgttttta taaacgaggc 300
cgtttttttg cccgcaaagt tactgtttgc gatgtaagat caaaaagggtg aatcatttca 360
gcacagtgtg tattgtgtaa agtcattccta aaagcttattc tattgattcc gaaatattgt 420
aatgtgtaca ctttttggac atacctgcat gttatatgat gaaatagaaa tgaaataaat 480
ggaaaaggag ttgttttaaa atg aag gtc aat aaa tta tta act ggt acg act 533
Met Lys Val Asn Lys Leu Leu Thr Gly Thr Thr
1 5 10
ctg gct gtt ggt tta ctt att tct gca gcg ccg gta ttt gct gca tcg 581
Leu Ala Val Gly Leu Leu Ile Ser Ala Ala Pro Val Phe Ala Ala Ser
15 20 25
cat tca tct gag gtg att gca cat ccg act gct caa tat atc aat tgt 629
His Ser Ser Glu Val Ile Ala His Pro Thr Ala Gln Tyr Ile Asn Cys
30 35 40
cca agt gac ttg cca agc tca ttc aaa agc agt aaa tca tca aaa tgt 677
Pro Ser Asp Leu Pro Ser Ser Phe Lys Ser Ser Lys Ser Ser Lys Cys
45 50 55
gta aaa tca tct tct gga gtt ttc agt aac aaa ttt tct gat agc gat 725
Val Lys Ser Ser Ser Gly Val Phe Ser Asn Lys Phe Ser Asp Ser Asp
60 65 70 75
gga aca tgg tat ttc aaa ggg aaa ttt tac agt aat gtt ttt aat act 773
Gly Thr Trp Tyr Phe Lys Gly Lys Phe Tyr Ser Asn Val Phe Asn Thr
80 85 90
tgg gtt ggt ttt tat gaa gga tgaacaaaa aaggggggct cccctttttt 824

Trp Val Gly Phe Tyr Glu Gly
95

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agatcttcgc	tatccggtga	attttttcgg	gccaggggtg	aggattaacc	attacggatt	1004
gctcatcgta	aacagcaatg	caaaaatagg	tgcaaactgt	gacattcatc	aaggggttaa	1064
tatcggacaa	aatcacgctc	gccgcgatgt	tcccacaatc	ggagacaatg	tctggatcgg	1124
gccgggggca	aagctctttg	gcgacattca	cattgctgac	ggcatatcaa	ttggcgcaaa	1184
cgccgtggtc	aacaaatctt	tcactgagga	aaatattaca	atagccggca	tgccctgccaa	1244
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<210> 138

<211> 98

<212> PRT

<213> Bacillus licheniformis

<400> 138

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			20					25					30		
Ile	Ala	His	Pro	Thr	Ala	Gln	Tyr	Ile	Asn	Cys	Pro	Ser	Asp	Leu	Pro
		35					40				45				
Ser	Ser	Phe	Lys	Ser	Ser	Lys	Ser	Ser	Lys	Cys	Val	Lys	Ser	Ser	Ser
	50					55					60				
Gly	Val	Phe	Ser	Asn	Lys	Phe	Ser	Asp	Ser	Asp	Gly	Thr	Trp	Tyr	Phe
65					70				75						80
Lys	Gly	Lys	Phe	Tyr	Ser	Asn	Val	Phe	Asn	Thr	Trp	Val	Gly	Phe	Tyr
				85					90					95	
Glu	Gly														

<210> 139

<211> 1261

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(836)

<223>

<400> 139

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acggctatca aagatttgac acgctgacga tgatcatcac ggttgcaatt ctcgatcatcg      420
tagtgcaagg attgcagaca tccggaaacg ttctgtcaaa aaaattgaga agaagataga      480
cagagagggg gacggctatt atg aaa aaa ttt gca tgt gtt gtg atc ttc ctg      533
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                        1         5         10

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Leu Leu Ala Ala Val Ile Ala Gly Cys Ala Ala Asp Ser Asp Ala Lys
                        15         20         25

acc att aaa atc ggc atc agc gga acg gat acg aga att tgg gac ttt      629
Thr Ile Lys Ile Gly Ile Ser Gly Thr Asp Thr Arg Ile Trp Asp Phe
                        30         35         40

gtg aag aaa aaa gcc gaa aaa gaa ggc tta aag ctt gaa atc gtc aaa      677
Val Lys Lys Lys Ala Glu Lys Glu Gly Leu Lys Leu Glu Ile Val Lys
                        45         50         55

tac tcc gac tat gtt cag cca aac cag gct ttg gcg agc ggc gac att      725
Tyr Ser Asp Tyr Val Gln Pro Asn Gln Ala Leu Ala Ser Gly Asp Ile
60                        65                        70                        75

gac cgc caa cgc ttt tca gac gat atc cta ctt tca tgc att caa aaa      773
Asp Arg Gln Arg Phe Ser Asp Asp Ile Leu Leu Ser Cys Ile Gln Lys
                        80                        85                        90

gga acg caa cct tta att atc gcc ggt cgg cac aac gac acc agg tcg      821
Gly Thr Gln Pro Leu Ile Ile Ala Gly Arg His Asn Asp Thr Arg Ser
                        95         100        105

ggg ggg gga gga aga ataaataaac acgggccctt ttggttgata agtccccggc      876
Gly Gly Gly Gly Arg
110

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gcaatcagcg ccggaaagct gaatgacaag gcgcagatca gcgtgccggc cgtaaataaa     1056
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IO294.000.ST25.txt

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gtaatgttta agtccctcat aatcggaggc agagccctga tgaatcccct aatgattttg 1236
gtaaaaaatca ttaagttaag gtgga 1261

<210> 140

<211> 112

<212> PRT

<213> Bacillus Ticheniformis

<400> 140

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20 25 30
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35 40 45
Glu Lys Glu Gly Leu Lys Leu Glu Ile Val Lys Tyr Ser Asp Tyr Val
50 55 60
Gln Pro Asn Gln Ala Leu Ala Ser Gly Asp Ile Asp Arg Gln Arg Phe
65 70 75 80
Ser Asp Asp Ile Leu Leu Ser Cys Ile Gln Lys Gly Thr Gln Pro Leu
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100 105 110

<210> 141

<211> 1426

<212> DNA

<213> Bacillus Ticheniformis

<220>

<221> CDS

<222> (507)..(923)

<223>

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aaggaaaaag tatagaggaa ttgcag gtg att gta aag acg gat cga ttc att      533
                        Val Ile Val Lys Thr Asp Arg Phe Ile
                        1 5
ttc acg agt cat tcc aag tcc att ata ttc cca atc gcc agt ttt tct      581
Phe Thr Ser His Ser Lys Ser Ile Ile Phe Pro Ile Ala Ser Phe Ser
10 15 20 25
ttt ata ttg gct aag cta agc aca gat gtg cat acc tgt gcg ctt ttg      629
Phe Ile Leu Ala Lys Leu Ser Thr Asp Val His Thr Cys Ala Leu Leu
30 35 40
gag gtg tgc tca ttt gca gag cac tca act gct caa att gta tat atc      677
Glu Val Cys Ser Phe Ala Glu His Ser Thr Ala Gln Ile Val Tyr Ile
45 50 55
ctc ccg ccg gaa cag gct ttt att gac ctt ttt tct gat ccg acc ggc      725
Leu Pro Pro Glu Gln Ala Phe Ile Asp Leu Phe Ser Asp Pro Thr Gly
60 65 70
cgt ttt gtc ttt cac ccc cgt tca tat ccg gga cgc tgc cct tcc ccc      773
Arg Phe Val Phe His Pro Arg Ser Tyr Pro Gly Arg Cys Pro Ser Pro
75 80 85
tct ccc gga tcg gcc ttc tcg aaa ttc agc gga ttt gct tat ttg atg      821
Ser Pro Gly Ser Ala Phe Ser Lys Phe Ser Gly Phe Ala Tyr Leu Met
90 95 100 105
cct atg gtc tct cgc tct cgt ccc tat gct gtt gtt tta cgt tac ttc      869
Pro Met Val Ser Arg Ser Arg Pro Tyr Ala Val Val Leu Arg Tyr Phe
110 115 120
aaa tgt ctg ccg ggc tct ccg cgt ccc acg cca cca aac aaa cgg ggt      917
Lys Cys Leu Pro Gly Ser Pro Arg Pro Thr Pro Pro Asn Lys Arg Gly
125 130 135
ctc ccc tgattttcgt cggctgcccc tctctgcttt ttgattaccc cccttctctt      973
Leu Pro

attgaagccc gcctcggctg gtttccatcg tccgctacgc gccgcaaattg ttatgctttt      1033
ctttatctaa aggctctacc cttagtatct aactaacacc tgcattgcaca gaaatcggag      1093
tggctttgtg catgcaccga catcggagtg ggtctgtgca tgcaccgata tcggagagac      1153
tctgtgcatg caccgatatc ggagtggctc tgtgcatgca ccgatatcgg agtggctctg      1213
tgcattgcacc gatatcggag tggctctgtg catgcaccga tatcggagtg gctctcatgc      1273
acgtgttgat gaatgcggcc catgtacgtg ttgatgaatg cggcccatgt acgtgttgat      1333

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gaatgcggcc catgtacgtg ttgatgaatg cggccattct tatcagggga cccaacggg 1393
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<210> 142

<211> 139

<212> PRT

<213> Bacillus licheniformis

<400> 142

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Thr Asp Val His Thr Cys Ala Leu Leu Glu Val Cys Ser Phe Ala Glu
35 40 45

His Ser Thr Ala Gln Ile Val Tyr Ile Leu Pro Pro Glu Gln Ala Phe
50 55 60

Ile Asp Leu Phe Ser Asp Pro Thr Gly Arg Phe Val Phe His Pro Arg
65 70 75 80

Ser Tyr Pro Gly Arg Cys Pro Ser Pro Ser Pro Gly Ser Ala Phe Ser
85 90 95

Lys Phe Ser Gly Phe Ala Tyr Leu Met Pro Met Val Ser Arg Ser Arg
100 105 110

Pro Tyr Ala Val Val Leu Arg Tyr Phe Lys Cys Leu Pro Gly Ser Pro
115 120 125

Arg Pro Thr Pro Pro Asn Lys Arg Gly Leu Pro
130 135

<210> 143

<211> 1513

<212> DNA

<213> Bacillus licheniformis

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<221> CDS

<222> (496)..(1035)

<223>

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 aacaatgccc agtCaggagg tgatgaatga tgccatggat gtttttagtg atttccggaa 180
 tcgaagaggt tattGCCgcc atCgtatga aatatgtaga cggcacaaga aaaaaatggc 240
 cgattatcgt catGgtgttg gggtttggct tgtctttttt ctgcctttca aaagcaatgc 300
 agatgctatc agCCggtgtt gcatatgccg tatggaccgg aatcggcagc atcggcatta 360
 cggcagtcag tttatttttg ttttaaggagc gtattcgtgc tccgcagctc atctcgcttg 420
 gctttattat aatCGgggtg atcggcctgc gccttacatc atcttaaatt ttaatttgca 480
 ttggaggttg ctgat atg att aat cag ctt aaa ttg cgt ccg ctt gaa aga 531
 Met Ile Asn Gln Leu Lys Leu Arg Pro Leu Glu Arg
 1 5 10
 gaa gac ctt ccg ttt gtc cac cgt ctt aac aac gat gcg aaa att atg 579
 Glu Asp Leu Pro Phe Val His Arg Leu Asn Asn Asp Ala Lys Ile Met
 15 20 25
 tca tat tgg ttt gaa gaa ccg tac gag act ttt gtt gag ctg cag gat 627
 Ser Tyr Trp Phe Glu Glu Pro Tyr Glu Thr Phe Val Glu Leu Gln Asp
 30 35 40
 tta ttt gac aaa cac att cac gac caa agc gag cgg cgc ttt atc ata 675
 Leu Phe Asp Lys His Ile His Asp Gln Ser Glu Arg Arg Phe Ile Ile
 45 50 55 60
 gag aaa gag act gag atg atc gga ttg gta gag ctg gtc gaa att gat 723
 Glu Lys Glu Thr Glu Met Ile Gly Leu Val Glu Leu Val Glu Ile Asp
 65 70 75
 tat att cac agg cgg gcg gag ttt caa atc ata att gat ccc gag cat 771
 Tyr Ile His Arg Arg Ala Glu Phe Gln Ile Ile Ile Asp Pro Glu His
 80 85 90
 caa ggg aac ggt tat tgc tca agc gca aca tat ttg gca atg aac tac 819
 Gln Gly Asn Gly Tyr Ser Ser Ser Ala Thr Tyr Leu Ala Met Asn Tyr
 95 100 105
 gca ttt tcc gtc ttg aac ttg cac aaa ttg tat ttg atc gtc gac gaa 867
 Ala Phe Ser Val Leu Asn Leu His Lys Leu Tyr Leu Ile Val Asp Glu
 110 115 120
 gat aat gca aaa gcg att cac ttg tat aaa aag gca ggg ttc act atc 915
 Asp Asn Ala Lys Ala Ile His Leu Tyr Lys Lys Ala Gly Phe Thr Ile
 125 130 135 140
 gag agc gag ctg cag gat gaa ttt ttc gtc gac ggc tat tat cgt aac 963
 Glu Ser Glu Leu Gln Asp Glu Phe Phe Val Asp Gly Tyr Tyr Arg Asn
 145 150 155
 gcc att aga atg tgc att ttt cag gat gag ttt tta tca ctt aaa aaa 1011
 Ala Ile Arg Met Cys Ile Phe Gln Asp Glu Phe Leu Ser Leu Lys Lys
 160 165 170
 agc aaa gag gaa ggc atg cag gga taaataaaag agatggcggc gccatctcct 1065

10294.000.ST25.txt

Ser Lys Glu Glu Gly Met Gln Gly
175 180

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cgctatgcg aaggttttta tcagctgtga attccattgt tttttcttga ccgtcttcat 1245
caaaacCGgc cagttcatat ttgaagacgg agtattcctc gccgtcgtca aatttcgacg 1305
tgtcttcctc cccgtttcca gtaatgtgaa cataatatc gtccgtcccc acacggttta 1365
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<210> 144
<211> 180
<212> PRT
<213> Bacillus licheniformis

<400> 144

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Phe Val His Arg Leu Asn Asn Asp Ala Lys Ile Met Ser Tyr Trp Phe
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Glu Glu Pro Tyr Glu Thr Phe Val Glu Leu Gln Asp Leu Phe Asp Lys
35 40 45
His Ile His Asp Gln Ser Glu Arg Arg Phe Ile Ile Glu Lys Glu Thr
50 55 60
Glu Met Ile Gly Leu Val Glu Leu Val Glu Ile Asp Tyr Ile His Arg
65 70 75 80
Arg Ala Glu Phe Gln Ile Ile Ile Asp Pro Glu His Gln Gly Asn Gly
85 90 95
Tyr Ser Ser Ser Ala Thr Tyr Leu Ala Met Asn Tyr Ala Phe Ser Val
100 105 110
Leu Asn Leu His Lys Leu Tyr Leu Ile Val Asp Glu Asp Asn Ala Lys
115 120 125
Ala Ile His Leu Tyr Lys Lys Ala Gly Phe Thr Ile Glu Ser Glu Leu
130 135 140

Gln Asp Glu Phe Phe Val Asp Gly Tyr Tyr Arg Asn Ala Ile Arg Met
145 150 155 160

Cys Ile Phe Gln Asp Glu Phe Leu Ser Leu Lys Lys Ser Lys Glu Glu
165 170 175

Gly Met Gln Gly
180

<210> 145

<211> 1763

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (503)..(1264)

<223>

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ttgtcaataa	cttttctcaa	aattattttt	tggagctttt	tcattgtcagc	tgttttatcag										360	
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cttaagatga	attattgtta	tgtttctattt	taaacaagca	taggatgaaa	acaaagcagc										480	
atggacaagg	aggagttttt	ct	gtg aac	cat ttt	tat gtg	tgg cat	atc aaa								532	
			Val Asn	His Phe	Tyr Val	Trp His	Ile Lys									
			1		5		10									
cgg att aag cag cta atc att att atg ata gcc gct ttt gcg aca gca															580	
Arg Ile Lys Gln Leu Ile Ile Ile Met Ile Ala Ala Phe Ala Thr Ala																
			15					20					25			
agt ttt ttt tat gtg caa aac ctg ctc cct ctt cct gtg ttt tct aca															628	
Ser Phe Phe Tyr Val Gln Asn Leu Leu Pro Leu Pro Val Phe Ser Thr																
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gaa ggc gga gca aaa gcg gta tat aga gga gat tca gat aca aat gaa															676	
Glu Gly Gly Ala Lys Ala Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu																
		45					50				55					
gta gcc ctt aca ttt aat atc agc tgg gga gat caa aag gca atg ccc															724	
Val Ala Leu Thr Phe Asn Ile Ser Trp Gly Asp Gln Lys Ala Met Pro																
	60					65				70						

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75 80 85 90

cta tca gct tca tgg gca gag cgc cac ccg gat gtc gta gaa aga atc 820
Leu Ser Ala Ser Trp Ala Glu Arg His Pro Asp Val Val Glu Arg Ile
95 100 105

cgt aaa gat ggt cac cag atc ggg agt atg ggc tat gct tat aaa aac 868
Arg Lys Asp Gly His Gln Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn
110 115 120

tat tcg caa atg aag aaa agc gag atc aaa aaa gac tta gca aaa gca 916
Tyr Ser Gln Met Lys Lys Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala
125 130 135

cga cac tcc ttt caa aaa ctc ggg ctt gac gac ctt acg ctt tta aga 964
Arg His Ser Phe Gln Lys Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg
140 145 150

ccg ccg acc ggc cag ttt aat aaa gac gta ctc gat gtt gct aaa cag 1012
Pro Pro Thr Gly Gln Phe Asn Lys Asp Val Leu Asp Val Ala Lys Gln
155 160 165 170

tac ggc tac acc gtt gtt cat tat agt att aac tcg gat gac tgg acg 1060
Tyr Gly Tyr Thr Val Val His Tyr Ser Ile Asn Ser Asp Asp Trp Thr
175 180 185

aac ccg ggg gtt caa aag atc gtc caa aac gta aat gga acg gta aac 1108
Asn Pro Gly Val Gln Lys Ile Val Gln Asn Val Asn Gly Thr Val Asn
190 195 200

gcc ggt gac atc gtg ctc ttt cac gct tca gat tcc gcc aaa caa aca 1156
Ala Gly Asp Ile Val Leu Phe His Ala Ser Asp Ser Ala Lys Gln Thr
205 210 215

aaa gaa gcc ctg cca gag atc gtg cac cat ctc aga agc aag ggg ctc 1204
Lys Glu Ala Leu Pro Glu Ile Val His His Leu Arg Ser Lys Gly Leu
220 225 230

aaa aac gta aca gtc agc gaa tta atc gca aat acg gat gca aaa tct 1252
Lys Asn Val Thr Val Ser Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser
235 240 245 250

tca gaa gta aag tagcagccgg tctaagcgcg tgcctgaaat tttggcagca 1304
Ser Glu Val Lys

ttaaaagctg aaaagcggtg caggctaata aaggaagcag cattaatatag agccagtcct 1364
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<210> 146

<211> 254

<212> PRT

<213> *Bacillus licheniformis*

<400> 146

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Asn Leu Leu Pro Leu Pro Val Phe Ser Thr Glu Gly Gly Ala Lys Ala
35 40 45
Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu Val Ala Leu Thr Phe Asn
50 55 60
Ile Ser Trp Gly Asp Gln Lys Ala Met Pro Ile Leu Asp Thr Leu Lys
65 70 75 80
Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe Leu Ser Ala Ser Trp Ala
85 90 95
Glu Arg His Pro Asp Val Val Glu Arg Ile Arg Lys Asp Gly His Gln
100 105 110
Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn Tyr Ser Gln Met Lys Lys
115 120 125
Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala Arg His Ser Phe Gln Lys
130 135 140
Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg Pro Pro Thr Gly Gln Phe
145 150 155 160
Asn Lys Asp Val Leu Asp Val Ala Lys Gln Tyr Gly Tyr Thr Val Val
165 170 175
His Tyr Ser Ile Asn Ser Asp Asp Trp Thr Asn Pro Gly Val Gln Lys
180 185 190
Ile Val Gln Asn Val Asn Gly Thr Val Asn Ala Gly Asp Ile Val Leu
195 200 205
Phe His Ala Ser Asp Ser Ala Lys Gln Thr Lys Glu Ala Leu Pro Glu
210 215 220
Ile Val His His Leu Arg Ser Lys Gly Leu Lys Asn Val Thr Val Ser
225 230 235 240

Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser Ser Glu Val Lys
 245 250

<210> 147

<211> 1855

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (480)..(1346)

<223>

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 tggcaaatag tagtatgata tttgaaagac ggggtcccgt cgaatcgggt gaaaaacaaa 240
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 gccaaaggat ctttttttgt ttatcaggaa atttatgaaa attaaagact gctgaaacat 420
 aatcttaaca gtgcgaacct atactttggc aagagaagag caaaagggga gtggatgat 479
 gtg tca gct tta ttc aaa aaa ttg atg tta tct tca ttg atc ggg gtt 527
 Val Ser Ala Leu Phe Lys Lys Leu Met Leu Ser Ser Leu Ile Gly Val
 1 5 10 15
 tcc atc ggg tca gcg ctg ttt gca ccg aat gcg ggt gca caa gag ccg 575
 Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala Gly Ala Gln Glu Pro
 20 25 30
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 Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala His Arg Gly Ala Ser
 35 40 45
 gga tat gcg ccg gaa aac acg atg gct gct ttt gat aaa gcg ctt cag 671
 Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe Asp Lys Ala Leu Gln
 50 55 60
 atg aaa gca gat tat atc gag ctg gat gtt caa atg tcc aaa gac ggg 719
 Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln Met Ser Lys Asp Gly
 65 70 75 80
 gag ctt gtc atc att cac gat acg acc gta aac cgt acg aca gat att 767
 Glu Leu Val Ile Ile His Asp Thr Thr Val Asn Arg Thr Thr Asp Ile
 85 90 95
 gac tca gtg ctg ccg gtt gcc gta aag gat ttg acg ctt gcc gag ctg 815

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Arg	Lys	Leu	Asp	Ala	Gly	Ser	Phe	Phe	Gly	Pro	Gln	Phe	Ala	Gly	Glu	
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Arg	Ile	Pro	Thr	Phe	Glu	Glu	Val	Leu	Asp	Arg	Tyr	Lys	Gly	Lys	Val	
	130					135					140					
gga	atg	ctg	atc	gaa	ttg	aaa	gag	cct	gca	cgc	tat	ccg	gga	atc	gaa	959
Gly	Met	Leu	Ile	Glu	Leu	Lys	Glu	Pro	Ala	Arg	Tyr	Pro	Gly	Ile	Glu	
145					150					155					160	
gga	aaa	gtg	tca	gca	gca	ttg	aaa	gag	cgg	aga	atg	gat	aag	cct	aaa	1007
Gly	Lys	Val	Ser	Ala	Ala	Leu	Lys	Glu	Arg	Arg	Met	Asp	Lys	Pro	Lys	
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aac	gga	aaa	atc	att	gta	caa	tcg	ttt	gat	ttt	aac	tct	gtc	tat	aaa	1055
Asn	Gly	Lys	Ile	Ile	Val	Gln	Ser	Phe	Asp	Phe	Asn	Ser	Val	Tyr	Lys	
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Ile	His	Gln	Leu	Leu	Pro	Ser	Met	Pro	Thr	Gly	Val	Leu	Thr	Ser	Lys	
		195					200					205				
gcg	gcg	gac	tta	aca	gat	gca	aag	ctt	aag	gaa	ttt	tcc	ggc	tat	gcc	1151
Ala	Ala	Asp	Leu	Thr	Asp	Ala	Lys	Leu	Lys	Glu	Phe	Ser	Gly	Tyr	Ala	
	210					215					220					
aaa	tac	gtg	aac	gcc	aac	ttg	aaa	aat	gtg	gcc	gct	gat	cct	acg	ctt	1199
Lys	Tyr	Val	Asn	Ala	Asn	Leu	Lys	Asn	Val	Ala	Ala	Asp	Pro	Thr	Leu	
225					230					235					240	
gtg	ccg	aga	att	cat	gcg	ctc	ggc	atg	aag	ata	cgc	cct	tgg	acc	gtc	1247
Val	Pro	Arg	Ile	His	Ala	Leu	Gly	Met	Lys	Ile	Arg	Pro	Trp	Thr	Val	
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cgc	tcc	cgc	gat	gaa	gtg	cct	ccg	cta	ttt	agg	ccc	gcg	tgg	aac	ggg	1295
Arg	Ser	Arg	Asp	Glu	Val	Pro	Pro	Leu	Phe	Arg	Pro	Ala	Trp	Asn	Gly	
			260					265					270			
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Ile	Val	Thr	Asn	Phe	Pro	Asp	Tyr	Cys	Ser	Lys	Lys	Val	Arg	Glu	Pro	
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caa	taaaaaaccc tgaagtttgc tttgaagggc tttttaattt aaaaataaaa															1396
Gln																
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tgatacgcct	gaaaaattga	agaaatttgc	ggccaactac	ccgctcagtt	ttcaaaattg											1816
ggacttttta	accggatact	cgcaggaaga	aatcgaaaa													1855

<210> 148

<211> 289

<212> PRT

<213> Bacillus licheniformis

<400> 148

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 35 40 45

Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe Asp Lys Ala Leu Gln
 50 55 60

Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln Met Ser Lys Asp Gly
 65 70 75 80

Glu Leu Val Ile Ile His Asp Thr Thr Val Asn Arg Thr Thr Asp Ile
 85 90 95

Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu Thr Leu Ala Glu Leu
 100 105 110

Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro Gln Phe Ala Gly Glu
 115 120 125

Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg Tyr Lys Gly Lys Val
 130 135 140

Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg Tyr Pro Gly Ile Glu
 145 150 155 160

Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg Met Asp Lys Pro Lys
 165 170 175

Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe Asn Ser Val Tyr Lys
 180 185 190

Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly Val Leu Thr Ser Lys
 195 200 205

Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu Phe Ser Gly Tyr Ala
 210 215 220

Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala Ala Asp Pro Thr Leu
225 230 235 240

Val Pro Arg Ile His Ala Leu Gly Met Lys Ile Arg Pro Trp Thr Val
245 250 255

Arg Ser Arg Asp Glu Val Pro Pro Leu Phe Arg Pro Ala Trp Asn Gly
260 265 270

Ile Val Thr Asn Phe Pro Asp Tyr Cys Ser Lys Lys Val Arg Glu Pro
275 280 285

<210>	149
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<212>	DNA
<213>	<i>Bacillus licheniformis</i>

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<222> (501)..(1697)  
<223>
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		Met	Asn	Leu	Ile	Lys	Trp	Ile	Leu	Phe	Ser	Val				
		1				5					10					
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Ile	Ser	Phe	Ala	Phe	Phe	Gln	Pro	Ala	Pro	Ala	Ala	Leu	Leu	Lys	Glu	
			15					20					25			
aag	gac	gac	tat	act	att	ctt	gtt	tat	atg	att	ggt	tct	gac	atg	gaa	629
Lys	Asp	Asp	Tyr	Thr	Ile	Leu	Val	Tyr	Met	Ile	Gly	Ser	Asp	Met	Glu	
		30					35					40				

10294.000.ST25.txt

agc Ser	gat Asp	ttt Phe	cat His	atg Met	gca Ala	agc Ser	gat Asp	gac Asp	att Ile	cag Gln	gaa Glu	atg Met	atg Met	gat Asp	gcg Ala	677
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ggt Gly	tca Ser	tct Ser	tca Ser	aac Asn	gtc Val	aat Asn	gtc Val	gtt Val	ctt Leu	cag Gln	aca Thr	gga Gly	gga Gly	gca Ala	aaa Lys	725
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gtt Val	gaa Glu	cat His	cag Gln	aag Lys	ctg Leu	gtg Val	ccc Pro	ctc Leu	gaa Glu	aat Asn	gtc Val	ggg Gly	aag Lys	aaa Lys	aat Asn	821
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atg Met	gac Asp	agt Ser	ccc Pro	ggc Gly	tcc Ser	gtc Val	aca Thr	gat Asp	ttt Phe	atc Ile	aca Thr	tgg Trp	gga Gly	gtc Val	aaa Lys	869
		110					115					120				
aca Thr	tat Tyr	ccg Pro	gct Ala	aaa Lys	aaa Lys	tat Tyr	gta Val	ttg Leu	atc Ile	ttt Phe	tgg Trp	ggg Gly	cat His	ggg Gly	ctt Leu	917
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ggc Gly	tca Ser	gtt Val	gac Asp	ggc Gly	tac Tyr	ggg Gly	gga Gly	gac Asp	gaa Glu	aac Asn	ttc Phe	ggc Gly	aat Asn	aag Lys	aaa Lys	965
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acg Thr	aag Lys	caa Gln	aag Lys	ttt Phe	gat Asp	tta Leu	atc Ile	ggt Gly	ttt Phe	gac Asp	aac Asn	tgc Cys	aaa Lys	atg Met	gcc Ala	1061
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	205					210					215					
ctg Leu	cag Gln	tct Ser	gta Val	caa Gln	gac Asp	gac Asp	cct Pro	tca Ser	atc Ile	gat Asp	ccg Pro	aaa Lys	gag Glu	ctt Leu	ggc Gly	1205
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agg Arg	gaa Glu	atc Ile	gct Ala	gca Ala	ggc Gly	tac Tyr	gta Val	cag Gln	cag Gln	tca Ser	aaa Lys	gaa Glu	aac Asn	ggt Gly	gaa Glu	1253
				240				245						250		
aca Thr	gaa Glu	gac Asp	ctg Leu	cag Gln	cag Gln	tct Ser	tta Leu	att Ile	caa Gln	ttg Leu	aac Asn	cgt Arg	gtc Val	aaa Lys	gac Asp	1301
			255					260					265			
gct Ala	gtc Val	gat Asp	gcc Ala	ctc Leu	gac Asp	aga Arg	ttg Leu	agc Ser	gta Val	aac Asn	atg Met	aac Asn	ctg Leu	gca Ala	ttg Leu	1349
		270					275					280				
aaa Lys	gag Glu	cct Pro	gac Asp	gga Gly	aag Lys	cgc Arg	ctg Leu	ctc Leu	cac His	tac Tyr	gcg Ala	cgt Arg	ctc Leu	gct Ala	gct Ala	1397
	285					290					295					
gaa Glu	gat Asp	tat Tyr	gca Ala	gat Asp	gaa Glu	tcg Ser	gat Asp	atg Met	gtt Val	gat Asp	ttg Leu	gcg Ala	gat Asp	ttg Leu	tca Ser	1445
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10294.000.ST25.txt

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agc ttg atc ggt cag cag atc gga gcc gag aaa gaa gca aaa gag gtc 1493
Ser Leu Ile Gly Gln Gln Ile Gly Ala Glu Lys Glu Ala Lys Glu Val
320 325 330

gta aaa tcc gtc aag aag gct gtc atc atg aac atc aaa tct ccg gag 1541
Val Lys Ser Val Lys Lys Ala Val Ile Met Asn Ile Lys Ser Pro Glu
335 340 345

cat cca aga gga agc ggc atg tcc gtt tat tat ccg gcc aga gac aac 1589
His Pro Arg Gly Ser Gly Met Ser Val Tyr Tyr Pro Ala Arg Asp Asn
350 355 360

cat aag cgg ttt gcg gaa aaa tcg aaa ata tac cgc ctg ctt gac ttc 1637
His Lys Arg Phe Ala Glu Lys Ser Lys Ile Tyr Arg Leu Leu Asp Phe
365 370 375

agc agc cgg tat caa aca ttc atc aaa gat tac tcg cat tca aca ttt 1685
Ser Ser Arg Tyr Gln Thr Phe Ile Lys Asp Tyr Ser His Ser Thr Phe
380 385 390

aac ttt gat cta tagttgcgtt taacagcaaa aaagcgccgg cggaataacc 1737
Asn Phe Asp Leu

ggcacttttt ttatcggtc atgtgcttcc ggatcaatgg aagtcgtag atgatgaaag 1797
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gaatagaaga aattgcgacc tttttgttgt ccagccataa aaataaagga gtggcgcttg 1977
caatcagcaa gtaagcgaaa aacatatcca tgcgttttca gcccctttcg ataatgatag 2037
cgctgtcaaa aaaagcgga tgaaacatca attgtgtcta attggagaat attttgtgaa 2097
cattctgtta cttttattat accacgttct tcgaaaaatg atacatactg gaaagcattt 2157
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<210> 150

<211> 399

<212> PRT

<213> Bacillus licheniformis

<400> 150

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Ile Leu Val Tyr Met Ile Gly Ser Asp Met Glu Ser Asp Phe His Met
35 40 45

Ala Ser Asp Asp Ile Gln Glu Met Met Asp Ala Gly Ser Ser Ser Asn
50 55 60

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Val Asn Val Val Leu Gln Thr Gly Gly Ala Lys Lys Trp Ala Asn Pro
65 70 75 80

Ser Ile Ser His Lys Val Asn Gln Arg Trp Lys Val Glu His Gln Lys
85 90 95

Leu Val Pro Leu Glu Asn Val Gly Lys Lys Asn Met Asp Ser Pro Gly
100 105 110

Ser Val Thr Asp Phe Ile Thr Trp Gly Val Lys Thr Tyr Pro Ala Lys
115 120 125

Lys Tyr Val Leu Ile Phe Trp Gly His Gly Leu Gly Ser Val Asp Gly
130 135 140

Tyr Gly Gly Asp Glu Asn Phe Gly Asn Lys Lys Met Lys Ile Ser Glu
145 150 155 160

Leu Gln Ser Gly Ile Lys Thr Ala Tyr Glu His Thr Lys Gln Lys Phe
165 170 175

Asp Leu Ile Gly Phe Asp Asn Cys Lys Met Ala Gly Ile Glu Thr Ala
180 185 190

Tyr Ala Leu Arg Asp Tyr Gly Lys Tyr Met Leu Ala Ser Val Asp Tyr
195 200 205

Thr Asn Gln Asn Gly Trp Asp Tyr Lys Arg Ala Leu Gln Ser Val Gln
210 215 220

Asp Asp Pro Ser Ile Asp Pro Lys Glu Leu Gly Arg Glu Ile Ala Ala
225 230 235 240

Gly Tyr Val Gln Gln Ser Lys Glu Asn Gly Glu Thr Glu Asp Leu Gln
245 250 255

Gln Ser Leu Ile Gln Leu Asn Arg Val Lys Asp Ala Val Asp Ala Leu
260 265 270

Asp Arg Leu Ser Val Asn Met Asn Leu Ala Leu Lys Glu Pro Asp Gly
275 280 285

Lys Arg Leu Leu His Tyr Ala Arg Leu Ala Ala Glu Asp Tyr Ala Asp
290 295 300

Glu Ser Asp Met Val Asp Leu Ala Asp Leu Ser Ser Leu Ile Gly Gln
305 310 315 320

Gln Ile Gly Ala Glu Lys Glu Ala Lys Glu Val Val Lys Ser Val Lys
325 330 335

Lys Ala Val Ile Met Asn Ile Lys Ser Pro Glu His Pro Arg Gly Ser
 340 345 350

Gly Met Ser Val Tyr Tyr Pro Ala Arg Asp Asn His Lys Arg Phe Ala
 355 360 365

Glu Lys Ser Lys Ile Tyr Arg Leu Leu Asp Phe Ser Ser Arg Tyr Gln
 370 375 380

Thr Phe Ile Lys Asp Tyr Ser His Ser Thr Phe Asn Phe Asp Leu
 385 390 395

<210> 151

<211> 1170

<212> DNA

<213> Bacillus licheniformis

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<222> (501)..(674)

<223>

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 acgcctgaaa aagcgaaagc aagcctgaat cccaacgtaa aagttcagga gacgcgcctt 180
 gcttttagtca cgaacgagct ttcgcaagaa gtgctctgct acgaaattct cggcacgatt 240
 gaaaacgata cattccgcat gttcatcaat gccaatgacg gcacggaaga gaagggttcag 300
 aaaatgaaaa gcgcagaacc gatatacaac gacttgtaaa aacgatagat caaagggaaa 360
 aggcgataac atgccttttc ctttttagca ttcggaataa ttcgccctaa acatttccat 420
 actgaacata tgggcggaac gtccgcgggt aaattgaaaa tgcccggggc cataaatttt 480
 ccgggcagcg gaggaataat atg aaa aca atc gaa cgg tta tta ttt aag ata 533
 Met Lys Thr Ile Glu Arg Leu Leu Phe Lys Ile
 1 5 10
 ctc gtc gta cag acg gtc att tta atc agc gtg cag ctt ctt ttt cat 581
 Leu Val Val Gln Thr Val Ile Leu Ile Ser Val Gln Leu Leu Phe His
 15 20 25
 ttc tcc aag gct gag cct tat ctg tca aag gtc gtg cag tat gaa ggc 629
 Phe Ser Lys Ala Glu Pro Tyr Leu Ser Lys Val Val Gln Tyr Glu Gly
 30 35 40
 gtg aac aac atg aaa atc ggc gaa tgg atc gag aca ttt aag ccg 674

10294.000.ST25.txt

Val Asn Asn Met Lys Ile Gly Glu Trp Ile Glu Thr Phe Lys Pro
45 50 55

taattcacgc taaaatctcc cctttttcgc ctaatacatg atacaatcct ataaggagta 734
ccagatagca aggagaggaa ttatggaaaa gaaattatgc attgcaatag acggccctgc 794
ggcagccgga aaaagcaccg tggcgaaaat cgtggccaga aaaaagtcgt atatttatat 854
tgatacgggt gccatgtaca gggcgattac gtatctagcg ctggaaaagg gcgttgattt 914
aaacgacgaa gcggcgctga cggccttggt aaaagaatct gccatcgatc tcacggtttc 974
gcctgaagga gagcagaagg tttatatcgc aggcgaagat gtaacagagg cgatccgcac 1034
ggatagcgtg agcaaccaag tctccatcgt cgccaaatac gccgggatcc gcgaagaaat 1094
gacgaaaagg cagcagcagc tggctgaaaa aggcgaggtc gtcatggacg gccgcgacat 1154
cggaaccac gttctc 1170

<210> 152
<211> 58
<212> PRT
<213> Bacillus licheniformis

<400> 152
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Val Ile Leu Ile Ser Val Gln Leu Leu Phe His Phe Ser Lys Ala Glu
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Pro Tyr Leu Ser Lys Val Val Gln Tyr Glu Gly Val Asn Asn Met Lys
35 40 45

Ile Gly Glu Trp Ile Glu Thr Phe Lys Pro
50 55

<210> 153
<211> 1435
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(932)
<223>

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aatcgaaagg tgcggtaaag agctttgtcg accgccatgg cttactttt ccggtcgctt 1392
tggatcaatc ggctgaagtt taccgttctt gggaaatgta tta 1435

<210> 154

<211> 144

<212> PRT

<213> Bacillus licheniformis

<400> 154

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Gly Ile His Ile Gln Pro Ala Glu Ala Ala Val Ile Lys Asp Glu Lys
20 25 30

Lys Met Thr Met Thr Met Thr Glu Asp His Val Gly Phe Phe Met Ala
35 40 45

Asp Ser Thr Asn Val Asn Tyr Tyr Pro Thr Trp Leu Tyr Tyr Lys Leu
50 55 60

Thr Ile Phe Asn Ala Glu Gly Cys Thr Leu Asn Ile Lys Leu Gln Arg
65 70 75 80

Ile Thr Leu Thr Gly His Ala Val Thr Leu Ser Glu Lys Glu Tyr Thr
85 90 95

Gly Asn His Leu His Leu Ser Ala Ala Asp Lys Val Ser Gly Ser Pro
100 105 110

His Arg Asn His Phe Leu Asp Ile Thr Lys Val Ser Gly Cys Gly Asp
115 120 125

Val Gly Ile Thr Gly Phe Tyr Gly Phe Glu His Gln Met Pro Gly Tyr
130 135 140

<210> 155

<211> 1768

<212> DNA

<213> Bacillus licheniformis

<220>

<223>

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Thr Trp Phe Gln Leu Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val
175 180 185

gcc att atg aaa tac aat tca ggc ggc aaa gtg aca gta agt gca agc 1109
Ala Ile Met Lys Tyr Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser
190 195 200

act tat atg aac ggt gat acg tcc gga gtg atc aga aat aat gac gaa 1157
Thr Tyr Met Asn Gly Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu
205 210 215

tac atc aga acg acc gtc aca aaa cag aga aaa ccg tcc aat aat aaa 1205
Tyr Ile Arg Thr Thr Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys
220 225 230 235

agc tca ggc ggc gga acg acg agc gga ggc cat tcg cac agc ggc agc 1253
Ser Ser Gly Gly Gly Thr Thr Ser Gly Gly His Ser His Ser Gly Ser
240 245 250

cgg gga agc ttt tagaaagggg aaggaagagc ttaaattggtg ttttttagaa 1305
Arg Gly Ser Phe
255

atcaatttgc aaatgtagta gagtgggatg aatttcgcga tgatatgatt ttctataaat 1365
ggaacaaccg cgaaatcaaaa aaggggagcc ggctgatcat tcgccccggt caggatgccg 1425
tcttttttaa caacggaaaa attgaaggca ttttccagga tgagggacgac tatgatattg 1485
aatccgaaat tattcctttt ttatccactt taaaagggtt taaatttggtc tttaacagcg 1545
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agaatgccat caatatcccc gctgcaggac ttccgggagg catgccgatc agggcgaacg 1665
gaagatttaa ctttaagggtg aatgattatg tcgcattaat cgataaaaatt gccggtgtga 1725
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<210> 156

<211> 255

<212> PRT

<213> Bacillus licheniformis

<400> 156

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20 25 30

Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys Gln Glu Ile Glu Lys
35 40 45

Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu Arg Glu Thr Asp Phe
50 55 60

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Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg Asp Val Lys Lys Tyr
65          70          75          80

Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly Tyr Gln Lys Lys His
85          90          95

Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu His Arg Glu Val Tyr
100         105         110

Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu Asn Asp Ala Arg Leu
115         120         125

Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile Ser Asp Lys His Tyr
130         135         140

Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala His Asp Asp Met Glu
145         150         155         160

Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys Thr Trp Phe Gln Leu
165         170         175

Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val Ala Ile Met Lys Tyr
180         185         190

Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser Thr Tyr Met Asn Gly
195         200         205

Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu Tyr Ile Arg Thr Thr
210         215         220

Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys Ser Ser Gly Gly Gly
225         230         235         240

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<210> 157

<211> 1688

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1652)

<223>

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		Met Arg Phe Phe	Leu Lys Gln Ala Ala Ala															
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atc atg ata tgc tct ctt tta tgc tct tca tac gaa acc gct caa gca											581							
Ile Met Ile Cys Ser Leu Leu Cys Ser Ser Tyr Glu Thr Ala Gln Ala																		
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cag ccc tcc ctt cat atc agc gca aaa agc gcg att gtc atg gac ggg											629							
Gln Pro Ser Leu His Ile Ser Ala Lys Ser Ala Ile Val Met Asp Gly																		
		30		35	40													
caa tcc gga cgg gtt ttg ttt gca aag gat gag cat gaa aaa cgg cgc											677							
Gln Ser Gly Arg Val Leu Phe Ala Lys Asp Glu His Glu Lys Arg Arg																		
		45		50	55													
att gca agc att acg aag att atg aca gcc att ttg gcc gtg gaa tcg											725							
Ile Ala Ser Ile Thr Lys Ile Met Thr Ala Ile Leu Ala Val Glu Ser																		
		60		65	70	75												
ggc aaa ttg gat gag acg gtc acg gtc agc gac aga gcg gtc agg aca											773							
Gly Lys Leu Asp Glu Thr Val Thr Val Ser Asp Arg Ala Val Arg Thr																		
		80		85	90													
gag gga tca tcg atc tat tta aca agc ggg caa aag gtg aag ctg aag											821							
Glu Gly Ser Ser Ile Tyr Leu Thr Ser Gly Gln Lys Val Lys Leu Lys																		
		95		100	105													
gac ctt gtt tac ggt ttg atg ctg aga tcg gga aat gat gca gcc gtt											869							
Asp Leu Val Tyr Gly Leu Met Leu Arg Ser Gly Asn Asp Ala Ala Val																		
		110		115	120													
gcg att gcc gaa cat gtg ggc gga agc ctg gaa ggc ttt gtc tac atg											917							
Ala Ile Ala Glu His Val Gly Gly Ser Leu Glu Gly Phe Val Tyr Met																		
		125		130	135													
atg aat caa aaa gcg gcc gag ctc ggc atg gaa aac acc ctg ttc cgc											965							
Met Asn Gln Lys Ala Ala Glu Leu Gly Met Glu Asn Thr Leu Phe Arg																		
		140		145	150	155												
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Asn Pro His Gly Leu Asp Asp His Pro Asp His Tyr Ser Ser Ala Tyr																		
		160		165	170													
gat atg gcg ctt tta aca aaa tat gcg atg agc aat gaa acg tac aaa											1061							
Asp Met Ala Leu Leu Thr Lys Tyr Ala Met Ser Asn Glu Thr Tyr Lys																		
		175		180	185													
aaa atc gcc gga acg aaa cgc tat aaa gca gaa acg atg caa ggc atc											1109							

10294.000.ST25.txt

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 Trp Glu Asn Lys Asn Lys Leu Leu Thr Gly Leu Tyr Lys Tyr Ser Thr
 205 210 215
 ggc ggg aag acg gga tat aca agg ctt gca aag cgg acg ctc gtc tcc 1205
 Gly Gly Lys Thr Gly Tyr Thr Arg Leu Ala Lys Arg Thr Leu Val Ser
 220 225 230 235
 att tca tcg aaa gac gga acc gat ttg atc gcc gtc aca atc aat gcc 1253
 Ile Ser Ser Lys Asp Gly Thr Asp Leu Ile Ala Val Thr Ile Asn Ala
 240 245 250
 cct gac gac tgg aat gat cat atg aac atg ttc aac tat gta ttc ggc 1301
 Pro Asp Asp Trp Asn Asp His Met Asn Met Phe Asn Tyr Val Phe Gly
 255 260 265
 cag tac aaa aca tat atc atc gcc aaa aaa ggc gag att ccg aaa tta 1349
 Gln Tyr Lys Thr Tyr Ile Ile Ala Lys Lys Gly Glu Ile Pro Lys Leu
 270 275 280
 aaa gac tct ttt tac gga cat aca gct ttt att aaa cgg gat gtc aca 1397
 Lys Asp Ser Phe Tyr Gly His Thr Ala Phe Ile Lys Arg Asp Val Thr
 285 290 295
 tat ctt tta aac gaa gag gaa aaa gaa gat gtg aag gtt gat atc gag 1445
 Tyr Leu Leu Asn Glu Glu Glu Lys Glu Asp Val Lys Val Asp Ile Glu
 300 305 310 315
 ctt ctt gaa ccg aaa aaa tca tgg cgt aaa aac aaa aaa gaa atc ccg 1493
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 320 325 330
 gac atc atc gga gaa atg aac gtc atg ttc gac gga aaa acg att gca 1541
 Asp Ile Ile Gly Glu Met Asn Val Met Phe Asp Gly Lys Thr Ile Ala
 335 340 345
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 Ser Val Pro Ile Tyr Tyr Glu Asn Glu Arg Asn Lys Asn Pro Lys Lys
 350 355 360
 tcg ttt ttc gag acc ttt caa tcc gta ttc caa aaa gcg gcg ggc ggt 1637
 Ser Phe Phe Glu Thr Phe Gln Ser Val Phe Gln Lys Ala Ala Gly Gly
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<210> 158

<211> 384

<212> PRT

<213> Bacillus licheniformis

<400> 158

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10294.000.ST25.txt

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 35 40 45
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 50 55 60
 Lys Ile Met Thr Ala Ile Leu Ala Val Glu Ser Gly Lys Leu Asp Glu
 65 70 75 80
 Thr Val Thr Val Ser Asp Arg Ala Val Arg Thr Glu Gly Ser Ser Ile
 85 90 95
 Tyr Leu Thr Ser Gly Gln Lys Val Lys Leu Lys Asp Leu Val Tyr Gly
 100 105 110
 Leu Met Leu Arg Ser Gly Asn Asp Ala Ala Val Ala Ile Ala Glu His
 115 120 125
 Val Gly Gly Ser Leu Glu Gly Phe Val Tyr Met Met Asn Gln Lys Ala
 130 135 140
 Ala Glu Leu Gly Met Glu Asn Thr Leu Phe Arg Asn Pro His Gly Leu
 145 150 155 160
 Asp Asp His Pro Asp His Tyr Ser Ser Ala Tyr Asp Met Ala Leu Leu
 165 170 175
 Thr Lys Tyr Ala Met Ser Asn Glu Thr Tyr Lys Lys Ile Ala Gly Thr
 180 185 190
 Lys Arg Tyr Lys Ala Glu Thr Met Gln Gly Ile Trp Glu Asn Lys Asn
 195 200 205
 Lys Leu Leu Thr Gly Leu Tyr Lys Tyr Ser Thr Gly Gly Lys Thr Gly
 210 215 220
 Tyr Thr Arg Leu Ala Lys Arg Thr Leu Val Ser Ile Ser Ser Lys Asp
 225 230 235 240
 Gly Thr Asp Leu Ile Ala Val Thr Ile Asn Ala Pro Asp Asp Trp Asn
 245 250 255
 Asp His Met Asn Met Phe Asn Tyr Val Phe Gly Gln Tyr Lys Thr Tyr
 260 265 270
 Ile Ile Ala Lys Lys Gly Glu Ile Pro Lys Leu Lys Asp Ser Phe Tyr
 275 280 285

Gly His Thr Ala Phe Ile Lys Arg Asp Val Thr Tyr Leu Leu Asn Glu
 290 295 300

Glu Glu Lys Glu Asp Val Lys Val Asp Ile Glu Leu Leu Glu Pro Lys
 305 310 315 320

Lys Ser Trp Arg Lys Asn Lys Lys Glu Ile Pro Asp Ile Ile Gly Glu
 325 330 335

Met Asn Val Met Phe Asp Gly Lys Thr Ile Ala Ser Val Pro Ile Tyr
 340 345 350

Tyr Glu Asn Glu Arg Asn Lys Asn Pro Lys Lys Ser Phe Phe Glu Thr
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Phe Gln Ser Val Phe Gln Lys Ala Ala Gly Gly Ser Ser Trp Ser Ile
 370 375 380

<210> 159

<211> 1617

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1118)

<223>

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 aattcagcgg gtgaggtggt cgacatgagg aaaggagtag tccttggttct gttcgctatg 180
 ctgttattgg caggctgcgg cacaacgcag cataatgggc aaagcgggtga tgagagccga 240
 aaaggaacag gcgaggaaac gctcgtgaaa gaaggcacct ttgtcgggttt ggcggaccag 300
 cataccgtcg ccgtcaatat tgacggcaaa gaaacgatgt ttcagggtccc tcccgaaaaa 360
 cgggacaaat ataaagggat cgaggatgat acaaaggtag aagtggagta cacgaaagca 420
 gaggacggaa cattacagct tgaagatatg aaaaagaaag aatgatcggt tgcaaaaagg 480
 gattgttagga ggaacaaatc gtg aaa ctg tta ata aag agt ttt gtt ttg ctg 533
 Val Lys Leu Leu Ile Lys Ser Phe Val Leu Leu
 1 5 10
 ctg ttt tcg ttt atg gcg gct ttt cca gct gct ttt gcg gct gag ccg 581
 Leu Phe Ser Phe Met Ala Ala Phe Pro Ala Ala Phe Ala Ala Glu Pro
 15 20 25

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ctt tcc ggg aag acg gta tat gtt gac gca ggt cac ggg ggt gaa gac Leu Ser Gly Lys Thr Val Tyr Val Asp Ala Gly His Gly Glu Asp 30 35 40	629
agc ggt gct gtc gga aac ggg ctg ctt gag aaa gat gtc aac ctt gaa Ser Gly Ala Val Gly Asn Gly Leu Leu Glu Lys Asp Val Asn Leu Glu 45 50 55	677
gtg gca atg ctg att gat gaa aag ctg aaa gaa gaa gga gcc gac aca Val Ala Met Leu Ile Asp Glu Lys Leu Lys Glu Glu Gly Ala Asp Thr 60 65 70 75	725
gtc gcc tca aga acg gat gat acg ttt ttg acg ctg gaa gac cgg gtg Val Ala Ser Arg Thr Asp Asp Thr Phe Leu Thr Leu Glu Asp Arg Val 80 85 90	773
gcc aag gcg agc aaa aat gct tca gac ttg ttt atc agc att cat gca Ala Lys Ala Ser Lys Asn Ala Ser Asp Leu Phe Ile Ser Ile His Ala 95 100 105	821
aac tcg gcc gtc cct gaa gcg tcc ggt aca gaa aca tat ttc gat tcc Asn Ser Ala Val Pro Glu Ala Ser Gly Thr Glu Thr Tyr Phe Asp Ser 110 115 120	869
acg tat caa gcc gct gac agc gaa cgg ctg gca tct gac att caa gag Thr Tyr Gln Ala Ala Asp Ser Glu Arg Leu Ala Ser Asp Ile Gln Glu 125 130 135	917
cgg ctt ccg gat gcg ctg ggc act cgg gac aga ggt gta aaa gaa tca Arg Leu Pro Asp Ala Leu Gly Thr Arg Asp Arg Gly Val Lys Glu Ser 140 145 150 155	965
ggg ttt tat gtc atc aaa aat tct caa atg ccg agt gtt tta gtc gaa Gly Phe Tyr Val Ile Lys Asn Ser Gln Met Pro Ser Val Leu Val Glu 160 165 170	1013
ctg ggc ttt atc aca aac aaa act gat gca gat aaa ctc gaa agt ccg Leu Gly Phe Ile Thr Asn Lys Thr Asp Ala Asp Lys Leu Glu Ser Pro 175 180 185	1061
gaa tat cag gaa aaa gct gca gac gcg att gct gac gct gtc gta tct Glu Tyr Gln Glu Lys Ala Ala Asp Ala Ile Ala Asp Ala Val Val Ser 190 195 200	1109
tat tat gaa taatagaagg gccctggtat atgaccgggg ttcttgtgtt Tyr Tyr Glu 205	1158
atgtttatgt taaaaaaggc cttatgtgtg gaaagaaaac agtaagacct tcataatggg	1218
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ggggccttcag gcacttttcc cgaaaataca atggcgggcgt ttaagcatgc ggcggccatt	1338
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catgatgaaa agcttgacag gacgacttca ctgaaaggggt atgtgaaaga tcttacatat	1458
gaggaaataa aacatggaga cgcaagccac cgttttgccg aaaaaaccgg ttctgtccct	1518
gtgccgaccc ttgaagaagt gtttgagtgg gcggcagatg ctgaatttct tcttaatgtt	1578
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<210> 160

<211> 206

<212> PRT

<213> Bacillus licheniformis

<400> 160

Val Lys Leu Leu Ile Lys Ser Phe Val Leu Leu Leu Phe Ser Phe Met
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Val Tyr Val Asp Ala Gly His Gly Gly Glu Asp Ser Gly Ala Val Gly
 35 40 45

Asn Gly Leu Leu Glu Lys Asp Val Asn Leu Glu Val Ala Met Leu Ile
 50 55 60

Asp Glu Lys Leu Lys Glu Glu Gly Ala Asp Thr Val Ala Ser Arg Thr
 65 70 75 80

Asp Asp Thr Phe Leu Thr Leu Glu Asp Arg Val Ala Lys Ala Ser Lys
 85 90 95

Asn Ala Ser Asp Leu Phe Ile Ser Ile His Ala Asn Ser Ala Val Pro
 100 105 110

Glu Ala Ser Gly Thr Glu Thr Tyr Phe Asp Ser Thr Tyr Gln Ala Ala
 115 120 125

Asp Ser Glu Arg Leu Ala Ser Asp Ile Gln Glu Arg Leu Pro Asp Ala
 130 135 140

Leu Gly Thr Arg Asp Arg Gly Val Lys Glu Ser Gly Phe Tyr Val Ile
 145 150 155 160

Lys Asn Ser Gln Met Pro Ser Val Leu Val Glu Leu Gly Phe Ile Thr
 165 170 175

Asn Lys Thr Asp Ala Asp Lys Leu Glu Ser Pro Glu Tyr Gln Glu Lys
 180 185 190

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 195 200 205

<210> 161

<211> 1803

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (165)..(1487)

<223>

<400> 161

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cattcctcct tgagagcggt ttcttaacaa acgggaggga tcgt atg aaa aag tta	176
Met Lys Lys Leu	
1	
tgt tgc ctg atc ttg gtc ttg gtt ttt tcc gcg ggc tgt act cag caa	224
Cys Cys Leu Ile Leu Val Leu Val Phe Ser Ala Gly Cys Thr Gln Gln	
5 10 15 20	
aag gca tca acg gaa gag gac ggg gcg ctt gaa atc aat tgg ctc gta	272
Lys Ala Ser Thr Glu Glu Asp Gly Ala Leu Glu Ile Asn Trp Leu Val	
25 30 35	
ccg ctc cac aca ccg cag cct ccg aaa gag aag gcg ctt gac atc att	320
Pro Leu His Thr Pro Gln Pro Pro Lys Glu Lys Ala Leu Asp Ile Ile	
40 45 50	
gaa gac aaa acg aat aca aag ctg aag ctc atc tgg gtt ccg gat tca	368
Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp Val Pro Asp Ser	
55 60 65	
aca aaa gaa gag cgg atc aat aca acc ctt gca agc gga aac atg cct	416
Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser Gly Asn Met Pro	
70 75 80	
aaa gta atg aca ttg cct gat ctt gaa gat tca gcg gtt gtc agc gcg	464
Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala Val Val Ser Ala	
85 90 95 100	
ctg cgc tcg gga atg ttc tgg gaa atc gga ccg tat ttc aaa gac tat	512
Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr Phe Lys Asp Tyr	
105 110 115	
ccg aat tta aga aaa ctt gat aaa act ata ttg aaa aat att tcg gtt	560
Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys Asn Ile Ser Val	
120 125 130	
gat ggc aaa gtt tac ggg att tat aga gaa agg ccg atg gcc agg cag	608
Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro Met Ala Arg Gln	
135 140 145	
gga gtc gtg att cgg aaa gac tgg ctc gac aat ctc gga ttg gaa atg	656
Gly Val Val Ile Arg Lys Asp Trp Leu Asp Asn Leu Gly Leu Glu Met	
150 155 160	
ccg gaa acc gtt gat gac ctt tat aaa ata gcg aaa gca ttt aca gaa	704
Pro Glu Thr Val Asp Asp Leu Tyr Lys Ile Ala Lys Ala Phe Thr Glu	
165 170 175 180	
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Arg	Asn	Asp	Leu 200	Thr	Phe	Gly	Ala	Phe 205	Lys	Thr	Leu	Ala	Ser 210	Tyr	Phe	
ggc	gcg	ccg	aac	gaa	tgg	gga	acg	gac	gaa	gac	gga	aat	ctc	ttc	ccc	848
Gly	Ala	Pro 215	Asn	Glu	Trp	Gly	Thr 220	Asp	Glu	Asp	Gly	Asn 225	Leu	Phe	Pro	
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Tyr	Phe 230	Lys	His	Glu	Ala	Tyr 235	Lys	Asp	Ala	Met	Ala 240	Tyr	Met	Lys	Lys	
ctt	tat	gaa	gaa	ggc	ctg	atg	aac	agg	gac	ttt	gcg	gtg	aca	agc	aaa	944
Leu 245	Tyr	Glu	Glu	Gly	Leu 250	Met	Asn	Arg	Asp	Phe 255	Ala	Val	Thr	Ser	Lys 260	
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Thr	Gln	Gln	Gln	Asp 265	Leu	Val	Ile	Gln	Gly 270	Lys	Ala	Gly	Ile	Tyr 275	Ile	
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Gly	Ala	Met	Ser 280	Asp	Ala	Met	Asn	Leu 285	Arg	Asp	Gln	Gly	Leu 290	Ala	Leu	
aac	ccc	ggc	ttt	cag	ctt	gat	atc	gca	aac	cgg	atc	aag	ggc	ccc	gac	1088
Asn	Pro	Gly 295	Phe	Gln	Leu	Asp	Ile 300	Ala	Asn	Arg	Ile	Lys 305	Gly	Pro	Asp	
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Gly	Lys 310	Glu	Arg	Thr	Trp	Ala 315	Leu	Gly	Gly	His	Gly 320	Gly	Met	Phe	Ala	
att	tcg	aaa	tca	agc	gtc	aag	act	gaa	aaa	gag	gtc	aga	aaa	atc	ctc	1184
Ile 325	Ser	Lys	Ser	Ser	Val 330	Lys	Thr	Glu	Lys	Glu 335	Val	Arg	Lys	Ile	Leu 340	
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Ala	Phe	Phe	Asp	Arg 345	Ile	Ala	Glu	Glu	Asp 350	Leu	Asn	Asn	Leu	Met 355	Leu	
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Tyr	Gly	Ile	Glu 360	Gly	Val	His	Tyr	Glu 365	Lys	Lys	Gly	Gly	Ser 370	Gly	Tyr	
ttt	cga	aag	cag	gaa	aac	tac	cat	ctg	tgg	gaa	gcg	gaa	att	cag	ccg	1328
Phe	Arg	Lys 375	Gln	Glu	Asn	Tyr	His 380	Leu	Trp	Glu	Ala	Glu 385	Ile	Gln	Pro	
tta	aac	cag	ctg	att	ggc	gtc	aat	aaa	caa	gct	tta	aaa	agc	gct	gaa	1376
Leu	Asn 390	Gln	Leu	Ile	Gly	Val 395	Asn	Lys	Gln	Ala	Leu 400	Lys	Ser	Ala	Glu	
gat	ccg	ctc	cg	gcc	aaa	aat	gaa	aag	ctt	gag	gag	gac	aac	cgg	gca	1424
Asp 405	Pro	Leu	Arg	Ala 410	Lys	Asn	Glu	Lys	Leu	Glu 415	Glu	Asp	Asn	Arg	Ala 420	
atc	gca	gtc	cag	aat	ccg	gcc	gaa	ccg	tgt	att	ctg	ccg	cac	aga	tgg	1472
Ile	Ala	Val	Gln	Asn 425	Pro	Ala	Glu	Pro	Cys 430	Ile	Leu	Pro	His	Arg 435	Trp	
aca	ggg	gaa	cag	aat	tga	a	a	a	a	a	a	a	a	a	a	1527
Thr	Gly	Glu	Gln 440	Asn												
cg	g	g	a	a	a	a	a	a	a	a	a	a	a	a	a	1587
g	g	g	a	a	a	a	a	a	a	a	a	a	a	a	a	

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 ttccattttt ttgaaaagga aagggttttt catcgtattc gctccaagtt cattttcttt 1707
 aaattctgca aaataaaca tataattcca tcataggacg aaaaggagga agcgatatgc 1767
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<210> 162

<211> 441

<212> PRT

<213> *Bacillus licheniformis*

<400> 162

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 35 40 45

Leu Asp Ile Ile Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp
 50 55 60

Val Pro Asp Ser Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser
 65 70 75 80

Gly Asn Met Pro Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala
 85 90 95

Val Val Ser Ala Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr
 100 105 110

Phe Lys Asp Tyr Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys
 115 120 125

Asn Ile Ser Val Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro
 130 135 140

Met Ala Arg Gln Gly Val Val Ile Arg Lys Asp Trp Leu Asp Asn Leu
 145 150 155 160

Gly Leu Glu Met Pro Glu Thr Val Asp Asp Leu Tyr Lys Ile Ala Lys
 165 170 175

Ala Phe Thr Glu Gln Asp Pro Asp Gln Asn Gly Lys Asp Asp Thr Phe
 180 185 190

Gly Leu Ala Asp Arg Asn Asp Leu Thr Phe Gly Ala Phe Lys Thr Leu
 195 200 205
 Ala Ser Tyr Phe Gly Ala Pro Asn Glu Trp Gly Thr Asp Glu Asp Gly
 210 215 220
 Asn Leu Phe Pro Tyr Phe Lys His Glu Ala Tyr Lys Asp Ala Met Ala
 225 230 235 240
 Tyr Met Lys Lys Leu Tyr Glu Glu Gly Leu Met Asn Arg Asp Phe Ala
 245 250 255
 Val Thr Ser Lys Thr Gln Gln Gln Asp Leu Val Ile Gln Gly Lys Ala
 260 265 270
 Gly Ile Tyr Ile Gly Ala Met Ser Asp Ala Met Asn Leu Arg Asp Gln
 275 280 285
 Gly Leu Ala Leu Asn Pro Gly Phe Gln Leu Asp Ile Ala Asn Arg Ile
 290 295 300
 Lys Gly Pro Asp Gly Lys Glu Arg Thr Trp Ala Leu Gly Gly His Gly
 305 310 315 320
 Gly Met Phe Ala Ile Ser Lys Ser Ser Val Lys Thr Glu Lys Glu Val
 325 330 335
 Arg Lys Ile Leu Ala Phe Phe Asp Arg Ile Ala Glu Glu Asp Leu Asn
 340 345 350
 Asn Leu Met Leu Tyr Gly Ile Glu Gly Val His Tyr Glu Lys Lys Gly
 355 360 365
 Gly Ser Gly Tyr Phe Arg Lys Gln Glu Asn Tyr His Leu Trp Glu Ala
 370 375 380
 Glu Ile Gln Pro Leu Asn Gln Leu Ile Gly Val Asn Lys Gln Ala Leu
 385 390 395 400
 Lys Ser Ala Glu Asp Pro Leu Arg Ala Lys Asn Glu Lys Leu Glu Glu
 405 410 415
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 Pro His Arg Trp Thr Gly Glu Gln Asn
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<210> 163

<211> 1400

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501) . . (983)

<223>

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cttttacact	gcaaaaaaaaa	aaaactatgt	aaaaaccata	tagaattata	tctaatttga			180								
tgtgaaatca	caatattttct	cgggaaaata	acatacacta	acgcctagaa	tcgataatta			240								
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actaatgaaa	cgcatttagg	gtacgataaa	aagtcgatgt	gagggtgagat	aagggtgtcaa			360								
ggcgcttttg	aaattgaagc	atctgctgga	taaagtgggtg	caatagcatg	taagctgccg			420								
gcatgaaacc	ggcagcattt	tttaagcgtc	cgacgggaag	tctttttttg	attaaatttc			480								
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		Met	Ser	Thr	Ile	Leu	Trp	Leu	Val	Ser	Phe	Thr				
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ctc	cac	ggt	ata	ttg	att	tat	ttc	gtc	atc	att	ttg	aat	acg	agg	ctc	581
Leu	His	Gly	Ile	Leu	Ile	Tyr	Phe	Val	Ile	Ile	Leu	Asn	Thr	Arg	Leu	
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agc	gct	ttc	aag	gca	gcg	gag	aaa	gag	caa	aaa	cag	ctt	ttg	gaa	gaa	629
Ser	Ala	Phe	Lys	Ala	Ala	Glu	Lys	Glu	Gln	Lys	Gln	Leu	Leu	Glu	Glu	
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acc	gag	aat	aca	ttg	acc	gct	ttt	ttg	atg	gag	tta	aaa	gac	gaa	aat	677
Thr	Glu	Asn	Thr	Leu	Thr	Ala	Phe	Leu	Met	Glu	Leu	Lys	Asp	Glu	Asn	
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gaa	aaa	ctc	gtt	caa	gag	att	cgg	gcg	aat	gcc	gaa	aaa	gag	ccg	caa	725
Glu	Lys	Leu	Val	Gln	Glu	Ile	Arg	Ala	Asn	Ala	Glu	Lys	Glu	Pro	Gln	
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aga	ccg	gaa	aca	cag	cct	gaa	att	ccc	gct	caa	acc	ccc	gtc	ctt	ccg	773
Arg	Pro	Glu	Thr	Gln	Pro	Glu	Ile	Pro	Ala	Gln	Thr	Pro	Val	Leu	Pro	
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gaa	gcg	gac	gaa	tcg	cgc	gat	ctg	ccg	ctt	cac	atc	gaa	gcg	atg	atc	821
Glu	Ala	Asp	Glu	Ser	Arg	Asp	Leu	Pro	Leu	His	Ile	Glu	Ala	Met	Ile	
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aat	gag	gtg	gag	cag	gaa	gag	gat	gag	ctc	aat	caa	aag	gag	cag	gaa	869
Asn	Glu	Val	Glu	Gln	Glu	Glu	Asp	Glu	Leu	Asn	Gln	Lys	Glu	Gln	Glu	
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gca	tcc	ata	tcc	tat	gaa	gaa	gaa	gct	ctc	gca	tta	gaa	aaa	cat	ggg	917

10294.000.ST25.txt

Ala	Ser	Ile	Ser	Tyr	Glu	Glu	Glu	Ala	Leu	Ala	Leu	Glu	Lys	His	Gly		
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Asp	Trp	Gly	Lys	Glu	Phe	Phe	His	Lys	Thr	Gly	Pro	Lys	Met	Gly	Gly		
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ggt	ggt	gtt	cca	gtc	tct	taaagaaaaa	aaaaattcaa	cctctcttct									1013
Gly	Gly	Val	Pro	Val	Ser												
				160													
ttggggagg	ggggggggga	aaaaataagg	tggttgtaga	ggggggaggga	atTTTTTTTT												1073
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tatcaagagg	gagccgcagg	gaggaaaata	caatccacgg	atcctaagtg	gtgagatgtc												1373
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<210> 164

<211> 161

<212> PRT

<213> Bacillus licheniformis

<400> 164

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Ala	Glu	Lys	Glu	Gln	Lys	Gln	Leu	Leu	Glu	Glu	Thr	Glu	Asn	Thr	Leu		
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Thr	Ala	Phe	Leu	Met	Glu	Leu	Lys	Asp	Glu	Asn	Glu	Lys	Leu	Val	Gln		
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Pro	Glu	Ile	Pro	Ala	Gln	Thr	Pro	Val	Leu	Pro	Glu	Ala	Asp	Glu	Ser		
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Arg	Asp	Leu	Pro	Leu	His	Ile	Glu	Ala	Met	Ile	Asn	Glu	Val	Glu	Gln		
			100					105					110				
Glu	Glu	Asp	Glu	Leu	Asn	Gln	Lys	Glu	Gln	Glu	Ala	Ser	Ile	Ser	Tyr		
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Glu Glu Glu Ala Leu Ala Leu Glu Lys His Gly Asp Trp Gly Lys Glu
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Phe Phe His Lys Thr Gly Pro Lys Met Gly Gly Gly Gly Val Pro Val
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Ser

<210> 165

<211> 2644

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (502)..(2142)

<223>

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Met Lys Ile Gln Lys Arg Val Gln Ala Leu
1 5 10
ctg gca act tcg gca atg ttt gca gga ctg atg ctg tcc gat gcg gtg 579
Leu Ala Thr Ser Ala Met Phe Ala Gly Leu Met Leu Ser Asp Ala Val
15 20 25
tac gct gcg gaa acc cct tac tat gga aag aac tat act cag cca gag 627
Tyr Ala Ala Glu Thr Pro Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu
30 35 40
caa gtg tca tca tta tat ccg gag cct gaa gaa aca ttc tca acc cct 675
Gln Val Ser Ser Leu Tyr Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro
45 50 55
gct ttt gta aaa gaa ggg gaa gcc ttt acg aca caa gaa gaa atg atg 723
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Ile Gln Asn Gly Ala Lys Val Ser Asp Lys Asp Gln Val Val Ile Asn
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Ser Glu Phe Ala Gly Pro Phe Lys Asp Thr Leu Lys Val Ala Asp Ile
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gcc tca gga caa gca gtt gac gtt cct gtc caa tat tac agc gcc tca 1731
Ala Ser Gly Gln Ala Val Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser
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gag gcc gtt cct gtg ctg tca aga act cgg ccg acc gct tac ctt gtc 1779
Glu Ala Val Pro Val Leu Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val
415 420 425

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Lys Ser Val Thr Leu Ala Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr
445 450 455

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Glu Val Leu Ser Lys Glu Thr Ala Gly Glu Ser Glu Gly Arg Pro Val
460 465 470

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Ile Lys Val Glu Thr Lys Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys
475 480 485 490

gga aca aaa atc tat ttt aca gct cag cag caa agc aat ctg ctg tca 2019
Gly Thr Lys Ile Tyr Phe Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser
495 500 505

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Ile Ala Leu Glu Pro Glu Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr
510 515 520

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525 530 535

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Asn Thr Lys Thr Leu Asn Phe Lys Glu
540 545

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Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe Thr Lys Asp Lys Gln Ile
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Arg Ser Ile Ser Lys Lys Pro Thr Val Trp Leu Gln Gly Gln Ile His
115 120 125

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145 150 155 160

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165 170 175

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180 185 190

Pro Glu Val Arg Ala Ile His Gln Glu Phe Asn Lys Tyr Ser Pro Glu
195 200 205

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 Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr His Asp Ile Leu Ile Leu
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 Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser Ile Arg His Ala Ser Asp
 245 250 255
 Ser Leu Tyr Val Asn Gly Val Arg Ala Lys Leu Asp Glu Lys Gly Phe
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 Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys Ser Lys Asp Gly Lys Ile
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 Glu Ile Tyr Glu Gly Gly Thr Glu Ala Arg Ile Gly Arg Asn Ala Phe
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 Ala Leu Gln Pro Ala Leu Ser Phe Leu Val Glu Ser Arg Gly Ile Asp
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 Ile Gly Arg Glu Asn Phe Ala Arg Arg Val Ala Ala Gln Val Ala Thr
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 465 470 475 480

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 Phe Lys Glu
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Glu	Pro	Val	Asp	Thr	Pro	Asp	Asp	Ala	Ala	Asp	Asp	Pro	Ala	Ile	Trp	
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Val	His	Pro	Lys	Gln	Pro	Glu	Lys	Ser	Arg	Leu	Ile	Thr	Thr	Asn	Lys	
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Lys	Ser	Gly	Leu	Ile	Val	Tyr	Asp	Leu	Asn	Gly	Lys	Gln	Leu	Ala	Ala	
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Tyr	Pro	Phe	Gly	Lys	Leu	Asn	Asn	Val	Asp	Leu	Arg	Tyr	Asn	Phe	Pro	
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Leu	Asp	Gly	Lys	Lys	Ile	Asp	Ile	Ala	Gly	Ala	Ser	Asn	Arg	Ser	Asp	
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ggc	aaa	aac	acg	gtt	gaa	ata	tac	gcc	ttt	gac	ggc	gaa	aaa	aac	aag	917
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Glu	Pro	Asn	Gly	Gly	Asp	Lys	Gly	Lys	Ile	Val	Asp	Arg	Ala	Gly	Gly	
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gcc	atc	tat	gac	cgg	cgc	ggg	aaa	aac	gac	tat	gtc	gcc	gat	ttt	tca	1397
Ala	Ile	Tyr	Asp	Arg	Arg	Gly	Lys	Asn	Asp	Tyr	Val	Ala	Asp	Phe	Ser	
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gtc gcc caa gac ggc gaa aat acg gaa aat gga cag cca gcc aat cag 1541
 Val Ala Gln Asp Gly Glu Asn Thr Glu Asn Gly Gln Pro Ala Asn Gln
 335 340 345

aac ttc aaa att gtc tcc tgg gaa aaa att gct gac gcg ctg gac gac 1589
 Asn Phe Lys Ile Val Ser Trp Glu Lys Ile Ala Asp Ala Leu Asp Asp
 350 355 360

aag cct gat atc gat gat cag gtc aat ccc cga aaa ctg aaa aaa cga 1637
 Lys Pro Asp Ile Asp Asp Gln Val Asn Pro Arg Lys Leu Lys Lys Arg
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gcc aaa taacgacgga tccgcgggaa atgcccgcgg atttttcaca ttcctttatg 1693
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ttaagataac tattaatgga gggatggtat tgcgtttaaa tctctatgcc gtagtggtta 1753

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<211> 381

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<213> Bacillus licheniformis

<400> 168

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 35 40 45

Pro Asp Asp Ala Ala Asp Asp Pro Ala Ile Trp Val His Pro Lys Gln
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Pro Glu Lys Ser Arg Leu Ile Thr Thr Asn Lys Lys Ser Gly Leu Ile
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 85 90 95
 Leu Asn Asn Val Asp Leu Arg Tyr Asn Phe Pro Leu Asp Gly Lys Lys
 100 105 110
 Ile Asp Ile Ala Gly Ala Ser Asn Arg Ser Asp Gly Lys Asn Thr Val
 115 120 125
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 Ser Leu Tyr His Ser Gln Lys Thr Gly Lys Phe Tyr Ala Met Val Thr
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 180 185 190
 Gly Gln Val Glu Gly Lys Lys Val Arg Ser Phe Lys Met Ser Ser Gln
 195 200 205
 Thr Glu Gly Leu Ala Ala Asp Asp Glu Tyr Gly Lys Met Tyr Ile Ala
 210 215 220
 Glu Glu Asp Ala Ala Ile Trp Ser Phe Ser Ala Glu Pro Asn Gly Gly
 225 230 235 240
 Asp Lys Gly Lys Ile Val Asp Arg Ala Gly Gly Pro His Leu Thr Ala
 245 250 255
 Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Gly Glu Asp Gly Glu Gly Tyr
 260 265 270
 Leu Ile Ala Ser Ser Gln Gly Asp Asn Arg Tyr Ala Ile Tyr Asp Arg
 275 280 285
 Arg Gly Lys Asn Asp Tyr Val Ala Asp Phe Ser Ile Asp Asp Gly Lys
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 Glu Ile Asp Gly Thr Ser Asp Thr Asp Gly Ile Asp Val Ile Gly Phe
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 Gly Leu Gly Lys Lys Tyr Pro Tyr Gly Ile Phe Val Ala Gln Asp Gly
 325 330 335

Glu Asn Thr Glu Asn Gly Gln Pro Ala Asn Gln Asn Phe Lys Ile Val
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Met Lys Arg Val Ile Val Leu Phe Ser Ile Leu	
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ctc gcc ctg ttc att gtt tat tat gac ttg aaa tca ggc acc atc cct	581
Leu Ala Leu Phe Ile Val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro	
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caa aac gcc tta ccg gct tca acc atg gca gcg gaa gct ccg gct gca	629
Gln Asn Ala Leu Pro Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala	
30 35 40	
agc ctg caa tat aag tcc gtt acg gta aag ccc gga caa acg gta ttt	677
Ser Leu Gln Tyr Lys Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe	
45 50 55	
tca atc atc ggg aac agc gcc gtt ccg gct gac aaa ata gcc gaa gat	725
Ser Ile Ile Gly Asn Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp	
60 65 70 75	

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ttt gaa gag ttg aat ccg aat gtt gag gcg ggc cgc att caa gca ggt 773
 Phe Glu Glu Leu Asn Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly
 80 85 90

gtc acc tac aag ttt ccc gtt tat cct gat taagcgtaa tttcttgtca 823
 Val Thr Tyr Lys Phe Pro Val Tyr Pro Asp
 95 100

gtttcatgaa cgggctgtta caataagact tgtaaacgat ttggtataag aaaaggagca 883

accgcctccg aattatactt aaggagcgaa ttcaagttag tgaaatcaca catcgtacaa 943

aaacgcgtcc cgtaaagtgt ggacctttta caataggcgg caataacgaa gtcgtcattc 1003

aaagcatgac aacaacgaaa acacatgacg ttgaagcaac cgtcgccgaa atcaacagac 1063

tcgcggaagc aggatgtcaa atcgtccgcg tcgcctgtcc tgatgaacgg gctgccgacg 1123

ccattccaga gatcaaaaag cggatatcca tccctcttgt cgtggatatt catttcaact 1183

ataaattggc attaaaagcg atcgaaggcg gagccgataa aatccgcac aatccgggta 1243

acatcggccg ccgcgaaaag gttgaagcgg tcgtcaacgc agcgaaggaa aagggcac 1301

<210> 170

<211> 101

<212> PRT

<213> Bacillus licheniformis

<400> 170

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Val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro Gln Asn Ala Leu Pro
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Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala Ser Leu Gln Tyr Lys
 35 40 45

Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe Ser Ile Ile Gly Asn
 50 55 60

Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp Phe Glu Glu Leu Asn
 65 70 75 80

Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly Val Thr Tyr Lys Phe
 85 90 95

Pro Val Tyr Pro Asp
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<210> 171

<211> 1627

<212> DNA

<213> Bacillus Ticheniformis

<220>

<221> CDS

<222> (501)..(1124)

<223>

[illegible]

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acg	gtg	acg	ctg	aag	aat	acc	ggc	ggc	agc	ttc	aaa	gta	acg	gat	atc	965
Thr	Val	Thr	Leu	Lys	Asn	Thr	Gly	Gly	Ser	Phe	Lys	Val	Thr	Asp	Ile	
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Gly	Gln	Ser	Asp	Thr	Lys	Pro	Ala	Gly	Glu	Glu	Ile	Met	Ser	Lys	Gln	
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ccg	gat	gaa	aaa	gaa	aca	agc	tcg	aat	ttt	gcg	gat	aaa	ggg	gaa	gga	1061
Pro	Asp	Glu	Lys	Glu	Thr	Ser	Ser	Asn	Phe	Ala	Asp	Lys	Gly	Glu	Gly	
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gac	cag	gct	gca	ttt	ccg	ctt	ttt	gcc	acc	gat	gtt	aac	tgg	aca	ttg	1109
Asp	Gln	Ala	Ala	Phe	Pro	Leu	Phe	Ala	Thr	Asp	Val	Asn	Trp	Thr	Leu	
		190					195					200				
gcc	gga	att	ttc	agc	tagcaaaaga	atttaaagaa	aatcattgac	aatgatactg								1164
Ala	Gly	Ile	Phe	Ser												
205																
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Arg	Ala	Ser	Leu	Phe	Glu	Thr	Leu	Gln	Ser	Val	Ser	Asp	Val	His	Phe	
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Gln	Leu	Thr	Glu	Lys	Glu	Arg	Thr	Lys	Thr	Asp	Met	Ile	Ser	Leu	Leu	
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Glu Pro Tyr Met Glu His Ala Met Ala Val Lys Tyr Val Glu Ala Asn
65 70 75 80

Ala Phe Pro Glu Gln Ala Gly Trp Ile Phe Tyr Gly Thr Asp Ala Pro
85 90 95

Glu Val Ala Ile Pro Phe Phe Ser Tyr Gly Gly Asp Thr Lys Val Ala
100 105 110

Gly Lys Asp Gly Ser Tyr Thr Val Tyr Glu Phe Val Gly Asp Gln Asn
115 120 125

Asp Gly Pro Val Ser Tyr Gln Lys Asn Tyr Gln Thr Val Thr Leu Lys
130 135 140

Asn Thr Gly Gly Ser Phe Lys Val Thr Asp Ile Gly Gln Ser Asp Thr
145 150 155 160

Lys Pro Ala Gly Glu Glu Ile Met Ser Lys Gln Pro Asp Glu Lys Glu
165 170 175

Thr Ser Ser Asn Phe Ala Asp Lys Gly Glu Gly Asp Gln Ala Ala Phe
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Pro Leu Phe Ala Thr Asp Val Asn Trp Thr Leu Ala Gly Ile Phe Ser
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<210> 173

<211> 2297

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1802)

<223>

<400> 173
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tcccactacc ttgaaatgaa agcgcctggag aacaataagc ggcaagtgcct ccacgggtgct 180
aaagtcggct gcagcgcgat tatgctgact gacatttacc gatctcttat cggtgcaagc 240
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ggcgtgaaag gggttaaaat gtg aaa agg ttc ctt tca tct atc ttt atg gtc Val Lys Arg Phe Leu Ser Ser Ile Phe Met Val 1 5 10	533
acg gtc gct gta tgt ttg ctt tta tgc ggg tgc aag gcg agt cct gcc Thr Val Ala Val Cys Leu Leu Leu Ser Gly Cys Lys Ala Ser Pro Ala 15 20 25	581
tcc gat caa gcg gac ggc acc gaa ctg aca ttt tgg aca ttc aac ggc Ser Asp Gln Ala Asp Gly Thr Glu Leu Thr Phe Trp Thr Phe Asn Gly 30 35 40	629
ctt cat gaa cag ttt tat gct gag atg gtg aaa gaa tgg aac aaa aag Leu His Glu Gln Phe Tyr Ala Glu Met Val Lys Glu Trp Asn Lys Lys 45 50 55	677
tat ccc gag cga aaa atc aaa tta aat aca gtg gtg tat ccg tat gga Tyr Pro Glu Arg Lys Ile Lys Leu Asn Thr Val Val Tyr Pro Tyr Gly 60 65 70 75	725
cag atg cat gac aat tta tct atc tgc ctt tta gcc ggg aaa ggg gtt Gln Met His Asp Asn Leu Ser Ile Ser Leu Leu Ala Gly Lys Gly Val 80 85 90	773
cca gat att gcc gat gtt gag ctg ggg cgc tat tgc aac ttt ttg aag Pro Asp Ile Ala Asp Val Glu Leu Gly Arg Tyr Ser Asn Phe Leu Lys 95 100 105	821
ggc tct gac att cct ctt acc gat tta acg ccg ctt gtg gag gac gaa Gly Ser Asp Ile Pro Leu Thr Asp Leu Thr Pro Leu Val Glu Asp Glu 110 115 120	869
cgc gac aag ttt gtt gaa gcg agg ctg acg ctc tac agc aag aac ggc Arg Asp Lys Phe Val Glu Ala Arg Leu Thr Leu Tyr Ser Lys Asn Gly 125 130 135	917
aag ctt tac gga ctt gac aca cat gtc gga act acc gtg atg tat tac Lys Leu Tyr Gly Leu Asp Thr His Val Gly Thr Thr Val Met Tyr Tyr 140 145 150 155	965
aac atg gaa atg atg aat aaa gca ggc gtt gat ccg gac gac atc aaa Asn Met Glu Met Met Asn Lys Ala Gly Val Asp Pro Asp Asp Ile Lys 160 165 170	1013
aca tgg gaa gat tac agg gaa gcg ggc aaa aag gtc gtc aaa gct ctc Thr Trp Glu Asp Tyr Arg Glu Ala Gly Lys Lys Val Val Lys Ala Leu 175 180 185	1061
gga aag ccg atg acg acg att gaa acg acc gac ccg aat tca ttt ctg Gly Lys Pro Met Thr Thr Ile Glu Thr Thr Asp Pro Asn Ser Phe Leu 190 195 200	1109
ccg ctg gtt tcc cag cag gga tcc ggt tac ttt gat gag cag ggg cgg Pro Leu Val Ser Gln Gln Gly Ser Gly Tyr Phe Asp Glu Gln Gly Arg 205 210 215	1157
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cct gac ttg aaa ggg aaa atc gcg atc aga ccg ctg ccg gca tgg gaa Pro Asp Leu Lys Gly Lys Ile Ala Ile Arg Pro Leu Pro Ala Trp Glu	1397
gaa ggg gga gac cgc tca gcg gga atg ggc gga acg gcc acc gtg att Glu Gly Gly Asp Arg Ser Ala Gly Met Gly Gly Thr Ala Thr Val Ile	1445
cca aaa cag gcg aaa cag gtc gat ctg gcc aag gat ttc ttg aaa ttt Pro Lys Gln Ala Lys Gln Val Asp Leu Ala Lys Asp Phe Leu Lys Phe	1493
gcc aaa gcg tca aaa gaa ggc aac atc aag ctg tgg acc gtg ctc ggg Ala Lys Ala Ser Lys Glu Gly Asn Ile Lys Leu Trp Thr Val Leu Gly	1541
ttc gat ccg ctc aga tgg gat gtg tgg gac tcg gac gaa ttg aaa aaa Phe Asp Pro Leu Arg Trp Asp Val Trp Asp Ser Asp Glu Leu Lys Lys	1589
cca aat caa tat aca gaa tac ttt caa aac gga caa cac atc ttt tcc Pro Asn Gln Tyr Thr Glu Tyr Phe Gln Asn Gly Gln His Ile Phe Ser	1637
gtg ctt ctt gac ata aag gat gag atc aat ccg ctt tac ctt act gag Val Leu Leu Asp Ile Lys Asp Glu Ile Asn Pro Leu Tyr Leu Thr Glu	1685
gat tat gcg aag act tcc gat ctc gtc aac aga aac ata ctg tac gaa Asp Tyr Ala Lys Thr Ser Asp Leu Val Asn Arg Asn Ile Leu Tyr Glu	1733
gcg ctc aaa acg aag agc aaa aca ccg aaa gaa gca ttg gac aaa gca Ala Leu Lys Thr Lys Ser Lys Thr Pro Lys Glu Ala Leu Asp Lys Ala	1781
gca gct gaa gtg aaa ggg caa tagtctttca ttactgtaaa gcgaggcgat Ala Ala Glu Val Lys Gly Gln	1832
aacttgaaga ctgttaaaac agatacagtg cattcgtttc cgccggtgag cagaaaaaga	1892
aagatcagac gtttattata ttcagcaaaa gccgcaccct acattttttac agcacctttt	1952
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<210> 174

<211> 434

<212> PRT

<213> Bacillus licheniformis

<400> 174

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Leu Leu Leu Ser Gly Cys Lys Ala Ser Pro Ala Ser Asp Gln Ala Asp
 20 25 30

Gly Thr Glu Leu Thr Phe Trp Thr Phe Asn Gly Leu His Glu Gln Phe
 35 40 45

Tyr Ala Glu Met Val Lys Glu Trp Asn Lys Lys Tyr Pro Glu Arg Lys
 50 55 60

Ile Lys Leu Asn Thr Val Val Tyr Pro Tyr Gly Gln Met His Asp Asn
 65 70 75 80

Leu Ser Ile Ser Leu Leu Ala Gly Lys Gly Val Pro Asp Ile Ala Asp
 85 90 95

Val Glu Leu Gly Arg Tyr Ser Asn Phe Leu Lys Gly Ser Asp Ile Pro
 100 105 110

Leu Thr Asp Leu Thr Pro Leu Val Glu Asp Glu Arg Asp Lys Phe Val
 115 120 125

Glu Ala Arg Leu Thr Leu Tyr Ser Lys Asn Gly Lys Leu Tyr Gly Leu
 130 135 140

Asp Thr His Val Gly Thr Thr Val Met Tyr Tyr Asn Met Glu Met Met
 145 150 155 160

Asn Lys Ala Gly Val Asp Pro Asp Asp Ile Lys Thr Trp Glu Asp Tyr
 165 170 175

Arg Glu Ala Gly Lys Lys Val Val Lys Ala Leu Gly Lys Pro Met Thr
 180 185 190

Thr Ile Glu Thr Thr Asp Pro Asn Ser Phe Leu Pro Leu Val Ser Gln
 195 200 205

Gln Gly Ser Gly Tyr Phe Asp Glu Gln Gly Arg Leu Thr Leu Asn Asn
 210 215 220

Glu Thr Asn Val Lys Thr Leu Glu Phe Leu Lys Thr Leu Ile Glu Lys
 225 230 235 240

Asp Lys Ile Ala Val Thr Thr Pro Gly Gly Asn His His Ser Glu Glu
 245 250 255
 Tyr Tyr Gly Phe Met Asn Gln Gly Gly Ala Ala Ser Val Leu Met Pro
 260 265 270
 Ile Trp Tyr Met Gly Arg Phe Leu Asp Tyr Met Pro Asp Leu Lys Gly
 275 280 285
 Lys Ile Ala Ile Arg Pro Leu Pro Ala Trp Glu Glu Gly Gly Asp Arg
 290 295 300
 Ser Ala Gly Met Gly Gly Thr Ala Thr Val Ile Pro Lys Gln Ala Lys
 305 310 315 320
 Gln Val Asp Leu Ala Lys Asp Phe Leu Lys Phe Ala Lys Ala Ser Lys
 325 330 335
 Glu Gly Asn Ile Lys Leu Trp Thr Val Leu Gly Phe Asp Pro Leu Arg
 340 345 350
 Trp Asp Val Trp Asp Ser Asp Glu Leu Lys Lys Pro Asn Gln Tyr Thr
 355 360 365
 Glu Tyr Phe Gln Asn Gly Gln His Ile Phe Ser Val Leu Leu Asp Ile
 370 375 380
 Lys Asp Glu Ile Asn Pro Leu Tyr Leu Thr Glu Asp Tyr Ala Lys Thr
 385 390 395 400
 Ser Asp Leu Val Asn Arg Asn Ile Leu Tyr Glu Ala Leu Lys Thr Lys
 405 410 415
 Ser Lys Thr Pro Lys Glu Ala Leu Asp Lys Ala Ala Ala Glu Val Lys
 420 425 430

Gly Gln

<210> 175

<211> 1864

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (533)..(991)

<223>

<400> 175

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aaa	at	ac	gct	cat	ga	ac	gc	gcgt	gc	gc	gac	at	caac	tcaa	act	tga	240
cg	gcc	gct	ac	gag	ct	gat	ca	tccc	ct	ac	ct	ggat	gt	gctt	cat	attttccc	300
aac	gg	tc	gaa	gac	ttt	gc	ag	aaat	cg	gctt	cg	ct	at	gat	g	ataaaaaagc	360
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																Met	
																Tyr	
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ccg	agc	gac	ttt	gca	agc	gca	ctt	gaa	tct	tta	agc	tta	aaa	gac	atg		586
Pro	Ser	Asp	Phe	Ala	Ser	Ala	Leu	Glu	Ser	Leu	Ser	Leu	Lys	Asp	Met		
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aga	aaa	gcg	atc	cac	cg	ctt	ctt	gac	att	cg	gac	gaa	aat	acg	tgg		634
Arg	Lys	Ala	Ile	His	Arg	Leu	Leu	Asp	Ile	Arg	Asp	Glu	Asn	Thr	Trp		
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atg	ctg	ttc	ggc	act	ctg	ccg	ttt	tac	gcg	tgc	agc	cct	gat	cct	gaa		682
Met	Leu	Phe	Gly	Thr	Leu	Pro	Phe	Tyr	Ala	Cys	Ser	Pro	Asp	Pro	Glu		
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gat	cac	gcc	ctc	tta	cag	cg	ctg	cg	gaa	gcg	aaa	aac	gtc	acc	gtc		730
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Arg	Asn	Asp	Pro	Asp	Gly	Arg	Ser	Arg	Leu	Asn	Val	Asn	Ile	Phe	Asp		
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ggc	aat	atc	atc	gtg	acc	gat	ttc	gga	gat	act	ccg	ccg	ctc	ggc	aac		826
Gly	Asn	Ile	Ile	Val	Thr	Asp	Phe	Gly	Asp	Thr	Pro	Pro	Leu	Gly	Asn		
		85					90					95					
att	cag	aca	gac	agc	ctg	cca	agc	gcc	tac	gcg	aag	tgg	aga	aaa	aca		874
Ile	Gln	Thr	Asp	Ser	Leu	Pro	Ser	Ala	Tyr	Ala	Lys	Trp	Arg	Lys	Thr		
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gag	ctt	gcc	aaa	gaa	ctc	aac	tgc	cac	tgc	ccg	cac	gtc	cg	tgc	ctc		922
Glu	Leu	Ala	Lys	Glu	Leu	Asn	Cys	His	Cys	Pro	His	Val	Arg	Cys	Leu		
	115				120					125					130		
gga	ccg	aat	gtg	ctc	gtc	aaa	aac	agc	tat	tat	caa	gat	gtt	gat	ttt		970
Gly	Pro	Asn	Val	Leu	Val	Lys	Asn	Ser	Tyr	Tyr	Gln	Asp	Val	Asp	Phe		
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act	tcc	aga	aca	gca	aga	gta	tg	aaaa	aa	agc	aag	ccg	caa	gg	ctt	gcttt	1021
Thr	Ser	Arg	Thr	Ala	Arg	Val											
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 tct 1864

<210> 176

<211> 153

<212> PRT

<213> Bacillus licheniformis

<400> 176

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Asp Met Arg Lys Ala Ile His Arg Leu Leu Asp Ile Arg Asp Glu Asn
 20 25 30

Thr Trp Met Leu Phe Gly Thr Leu Pro Phe Tyr Ala Cys Ser Pro Asp
 35 40 45

Pro Glu Asp His Ala Leu Leu Gln Arg Leu Arg Glu Ala Lys Asn Val
 50 55 60

Thr Val Arg Asn Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Ile
 65 70 75 80

Phe Asp Gly Asn Ile Ile Val Thr Asp Phe Gly Asp Thr Pro Pro Leu
 85 90 95

Gly Asn Ile Gln Thr Asp Ser Leu Pro Ser Ala Tyr Ala Lys Trp Arg
 100 105 110

10294.000.ST25.txt

Lys Thr Glu Leu Ala Lys Glu Leu Asn Cys His Cys Pro His Val Arg
 115 120 125

Cys Leu Gly Pro Asn Val Leu Val Lys Asn Ser Tyr Tyr Gln Asp Val
 130 135 140

Asp Phe Thr Ser Arg Thr Ala Arg Val
 145 150

<210> 177

<211> 1763

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (503)..(1264)

<223>

<400> 177
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 Val Asn His Phe Tyr Val Trp His Ile Lys
 1 5 10
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 Arg Ile Lys Gln Leu Ile Ile Ile Met Ile Ala Ala Phe Ala Thr Ala
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 Ser Phe Phe Tyr Val Gln Asn Leu Leu Pro Leu Pro Val Phe Ser Thr
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 gaa ggc gga gca aaa gcg gta tat aga gga gat tca gat aca aat gaa 676
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10294.000.ST25.txt

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Arg	Lys	Asp	Gly	His	Gln	Ile	Gly	Ser	Met	Gly	Tyr	Ala	Tyr	Lys	Asn		
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Ser	Glu	Val	Lys														
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<211> 254

<212> PRT

<213> Bacillus licheniformis

<400> 178

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Asn Leu Leu Pro Leu Pro Val Phe Ser Thr Glu Gly Gly Ala Lys Ala
35 40 45
Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu Val Ala Leu Thr Phe Asn
50 55 60
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65 70 75 80
Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe Leu Ser Ala Ser Trp Ala
85 90 95
Glu Arg His Pro Asp Val Val Glu Arg Ile Arg Lys Asp Gly His Gln
100 105 110
Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn Tyr Ser Gln Met Lys Lys
115 120 125
Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala Arg His Ser Phe Gln Lys
130 135 140
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145 150 155 160
Asn Lys Asp Val Leu Asp Val Ala Lys Gln Tyr Gly Tyr Thr Val Val
165 170 175
His Tyr Ser Ile Asn Ser Asp Asp Trp Thr Asn Pro Gly Val Gln Lys
180 185 190
Ile Val Gln Asn Val Asn Gly Thr Val Asn Ala Gly Asp Ile Val Leu
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Phe His Ala Ser Asp Ser Ala Lys Gln Thr Lys Glu Ala Leu Pro Glu
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<212> DNA

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<222> (501) . . (1304)

<223>

<400> 179

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aggagtggga gaacaaaaa gagtaaaata cggagctgta tttctacagg agcttcaagc    240
ctataaaact gagaaagaag cataaaaacc caaaatttat atatgtaaaa ttttttttag    300
taaatctcct atttcagttg aaaaacgatt ggaacccttg atacatctga atttcggccg    360
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taacaaggga ggatttactt atg aag aag acg ttt atg tcc ttt gtt gca gtt    533
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gca gca tta tct tca act gca ttc gga gcg agt gcc tct gca aaa gaa      581
Ala Ala Leu Ser Ser Thr Ala Phe Gly Ala Ser Ala Ser Ala Lys Glu
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gta aca gtc caa aaa ggt gac acc ctt tgg gga atc tcg caa aaa caa      629
Val Thr Val Gln Lys Gly Asp Thr Leu Trp Gly Ile Ser Gln Lys Gln
                    30      35      40

ggg gta aat ctg cag gac tta aaa gaa tgg aat cag ctt tcc tct gac      677
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ttg att att ccg gga caa aag ctg aac gtt tct gaa aaa cag aca gaa      725
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gaa aag aaa caa tat acc att aaa aag gga gac act ctc tgg aaa atc      773
Glu Lys Lys Gln Tyr Thr Ile Lys Lys Gly Asp Thr Leu Trp Lys Ile
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<211> 268

<212> PRT

<213> Bacillus licheniformis

<400> 180

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 50 55 60
 Gln Lys Leu Asn Val Ser Glu Lys Gln Thr Glu Glu Lys Lys Gln Tyr
 65 70 75 80
 Thr Ile Lys Lys Gly Asp Thr Leu Trp Lys Ile Ala Gln Lys Phe Gly
 85 90 95
 Val Ser Val Asn Asp Leu Lys Asn Trp Asn Asn Ile Lys Ser Asp Ile
 100 105 110
 Ile Tyr Pro Asn Thr Ser Ile Thr Val Asp Gly Gln Ala Thr Val Gln
 115 120 125
 Ala Ala Ala Ala Gln Pro Ala Glu Thr Lys Pro Ala Val Gln Lys Glu
 130 135 140
 Ala Lys Val Glu Lys Ala Ala Pro Ala Pro Ala Pro Lys Gln Glu Lys
 145 150 155 160
 Glu Pro Ala Ser Arg Ser Asn Val Ser Gln Ser Thr Ala Lys Glu Leu
 165 170 175
 Thr Val Thr Ala Thr Ala Tyr Thr Ala Asn Asp Gly Gly Met Thr Gly
 180 185 190
 Val Thr Ala Thr Gly Ile Asp Leu Lys Ala Asn Lys Asn Ala Lys Val
 195 200 205
 Ile Ala Val Asp Pro Asn Val Ile Pro Leu Gly Ser Lys Val Tyr Val
 210 215 220
 Glu Gly Tyr Gly Glu Ala Thr Ala Ala Asp Thr Gly Gly Ala Ile Lys
 225 230 235 240
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 Ser Gly Asn Leu Thr Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala
 30 35 40
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 Arg Glu His Phe Trp Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys
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 aac tca act tgc cca tcc aaa aca ttt gaa tac cgc ggt ctt cca tat 725
 Asn Ser Thr Cys Pro Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr
 60 65 70 75
 acg tat atg tgc agt gaa ttc agc aca aaa gca aaa tta aca gac tac 773
 Thr Tyr Met Cys Ser Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr
 80 85 90
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 Leu Thr Pro Val Phe Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys
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Gly Asp Asn Leu Leu Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser	
125 130 135	
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Gln Lys Asn Asn Thr Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp	
140 145 150 155	
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Gly Ser Val Thr Ala Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn	
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Lys Trp Lys Ile Asn Gln Leu Asp Ala Ala Ile	
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50 55 60	

Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr Thr Tyr Met Cys Ser
 65 70 75 80

Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr Leu Thr Pro Val Phe
 85 90 95

Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys Tyr Asn Ile Ile Ser
 100 105 110

Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp Gly Asp Asn Leu Leu
 115 120 125

Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser Gln Lys Asn Asn Thr
 130 135 140

Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp Gly Ser Val Thr Ala
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Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn Lys Trp Lys Ile Asn
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1

<211> 106

<213> Bacillus licheniformis

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Ala Glu Val Arg Leu Thr Lys Lys Val Trp Asp Arg Lys Arg Ala Asp
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Glu Ala Val Lys Gln Tyr His Val Thr Leu Ser Glu Gly Asn Lys Asn
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 10 15 20

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cct Pro 120	gtc Val	gaa Glu	cat His	cag Gln	ggg Gly	ttt Phe 125	ctc Leu	tgg Trp	tcg Ser	cta Leu	agc Ser 130	ggc Gly	tgg Trp	gac Asp	gtg Val	919
tat Tyr 135	gtc Val	act Thr	tgg Trp	gtg Val	ttg Leu 140	atc Ile	ggt Gly	tcg Ser	gga Gly	ggt Gly 145	gcg Ala	gtc Val	gtc Val	ctg Leu	aca Thr 150	967
gcg Ala	ctc Leu	aat Asn	tac Tyr	ttc Phe 155	ggc Gly	gtc Val	aag Lys	ccg Pro	gcc Ala 160	gcg Ala	att Ile	ttt Phe	cag Gln 165	tcg Ser 165	gtc Val	1015
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ttg Leu	gta Val	aac Asn 185	ggt Gly	gat Asp	ttc Phe	gaa Glu	cat His 190	gta Val	cag Gln	ccc Pro	ctt Leu	ttt Phe 195	aaa Lys	gac Asp	ggg Gly	1111
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gga Gly 215	ttt Phe	gac Asp	gtc Val	atc Ile	cct Pro 220	cag Gln	gtt Val	gcg Ala	gct Ala	gaa Glu 225	att Ile	aat Asn	gcc Ala	ccg Pro	aaa Lys 230	1207
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ttt Phe	tat Tyr	ttg Leu 250	ctg Leu	att Ile	gta Val	ttc Phe	ggc Gly	gta Val 255	acg Thr	atg Met	ggt Gly	ctg Leu	tca Ser 260	gaa Glu	agc Ser	1303
gag Glu	ctt Leu	gcg Ala 265	acg Thr	act Thr	tct Ser	ttg Leu	gca Ala 270	acc Thr	gcg Ala	gat Asp	gca Ala	atg Met 275	gtc Val	aat Asn	ctg Leu	1351
ctc Leu	ggg Gly 280	aac Asn	cag Gln	ctg Leu	ttc Phe	ggc Gly 285	acg Thr	gtg Val	ctt Leu	gtc Val	ctc Leu 290	ggc Gly	ggc Gly	gtc Val	gcc Ala	1399
gga Gly 295	atc Ile	att Ile	acg Thr	agc Ser	tgg Trp 300	aac Asn	gca Ala	ttt Phe	atc Ile	atc Ile 305	ggc Gly	gcg Ala	agc Ser	cgg Arg	att Ile 310	1447

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ctg ttt gca atg tcg gaa aag ggc atg gtg ccg aaa tgg ttc ggc ttc Leu Phe Ala Met Ser Glu Lys Gly Met Val Pro Lys Trp Phe Gly Phe 315 320 325	1495
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gcg ctg gcg ttt ttt gcc ccg ctg ctc gga cgc cct gcc ctt gtt tgg Ala Leu Ala Phe Phe Ala Pro Leu Leu Gly Arg Pro Ala Leu Val Trp 345 350 355	1591
atc gtc aat gca ggg gga aca ggt att ata gtc gga tat ttg atc gtc Ile Val Asn Ala Gly Gly Thr Gly Ile Ile Val Gly Tyr Leu Ile Val 360 365 370	1639
tcg att gca ttc atg aag ctg aga aaa aca gag ccg gat tta cac agg Ser Ile Ala Phe Met Lys Leu Arg Lys Thr Glu Pro Asp Leu His Arg 375 380 385 390	1687
ccg tat aaa atc aat aag tgg aaa aca acg ggt ata tct gct atc ctc Pro Tyr Lys Ile Asn Lys Trp Lys Thr Thr Gly Ile Ser Ala Ile Leu 395 400 405	1735
tta agt gtt atc ttc ctt gcc ttt tat ttg cca ggc atg ccg gcc gcg Leu Ser Val Ile Phe Leu Ala Phe Tyr Leu Pro Gly Met Pro Ala Ala 410 415 420	1783
ctc aca tgg ccg tat gag tgg ctg atc ttg gcg gga tgg aca ttg atc Leu Thr Trp Pro Tyr Glu Trp Leu Ile Leu Ala Gly Trp Thr Leu Ile 425 430 435	1831
ggt ttt ctt tta tac aac agc agt tca aaa cgt aaa ggg gag gag att Gly Phe Leu Leu Tyr Asn Ser Ser Ser Lys Arg Lys Gly Glu Glu Ile 440 445 450	1879
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ggtatgcgga ggaagcgaag cgcatctacg gaagaacggt tcccgccctct gtgacgaaca	2226
agcgcatcat cgtcacacgc cagggagtcg gacctgttgc ggcgattacc ccgtggaatt	2286
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<212> PRT

<213> Bacillus licheniformis

<400> 186

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 20 25 30
 Gly Asp Trp Ile Ser Thr Ala Gly Phe Leu Gly Ser Thr Ile Ala Phe
 35 40 45
 Ile Ile Gly Gly Ile Leu Val Ile Leu Ile Gly Leu Thr Tyr Ala Glu
 50 55 60
 Leu Ser Ser Ala Ile Pro Glu Thr Gly Gly Gly Leu Ile Phe Val Tyr
 65 70 75 80
 Arg Ala Phe Gly Arg Lys Thr Ala Phe Val Ala Ala Trp Gly Val Leu
 85 90 95
 Phe Gly Tyr Val Ser Val Ile Thr Phe Glu Ala Val Ala Leu Pro Thr
 100 105 110
 Val Ile Asp Tyr Val Leu Pro Val Glu His Gln Gly Phe Leu Trp Ser
 115 120 125
 Leu Ser Gly Trp Asp Val Tyr Val Thr Trp Val Leu Ile Gly Ser Gly
 130 135 140
 Gly Ala Val Val Leu Thr Ala Leu Asn Tyr Phe Gly Val Lys Pro Ala
 145 150 155 160
 Ala Ile Phe Gln Ser Val Phe Thr Ile Ala Ile Ile Ala Thr Gly Phe
 165 170 175
 Leu Leu Leu Gly Gly Ala Leu Val Asn Gly Asp Phe Glu His Val Gln
 180 185 190
 Pro Leu Phe Lys Asp Gly Phe Ser Gly Met Met Ser Val Leu Val Met
 195 200 205
 Ile Pro Phe Leu Phe Val Gly Phe Asp Val Ile Pro Gln Val Ala Ala
 210 215 220
 Glu Ile Asn Ala Pro Lys Lys Ile Ile Gly Lys Ile Leu Ile Ile Ser
 225 230 235 240
 Ile Ile Ser Ala Val Val Phe Tyr Leu Leu Ile Val Phe Gly Val Thr
 245 250 255
 Met Gly Leu Ser Glu Ser Glu Leu Ala Thr Thr Ser Leu Ala Thr Ala
 260 265 270

Asp Ala Met Val Asn Leu Leu Gly Asn Gln Leu Phe Gly Thr Val Leu
 275 280 285
 Val Leu Gly Gly Val Ala Gly Ile Ile Thr Ser Trp Asn Ala Phe Ile
 290 295 300
 Ile Gly Ala Ser Arg Ile Leu Phe Ala Met Ser Glu Lys Gly Met Val
 305 310 315 320
 Pro Lys Trp Phe Gly Phe Ile His Pro Lys Tyr Lys Thr Pro Thr Asn
 325 330 335
 Ala Ile Leu Phe Leu Gly Ala Leu Ala Phe Phe Ala Pro Leu Leu Gly
 340 345 350
 Arg Pro Ala Leu Val Trp Ile Val Asn Ala Gly Gly Thr Gly Ile Ile
 355 360 365
 Val Gly Tyr Leu Ile Val Ser Ile Ala Phe Met Lys Leu Arg Lys Thr
 370 375 380
 Glu Pro Asp Leu His Arg Pro Tyr Lys Ile Asn Lys Trp Lys Thr Thr
 385 390 395 400
 Gly Ile Ser Ala Ile Leu Leu Ser Val Ile Phe Leu Ala Phe Tyr Leu
 405 410 415
 Pro Gly Met Pro Ala Ala Leu Thr Trp Pro Tyr Glu Trp Leu Ile Leu
 420 425 430
 Ala Gly Trp Thr Leu Ile Gly Phe Leu Leu Tyr Asn Ser Ser Ser Lys
 435 440 445
 Arg Lys Gly Glu Glu Ile Gln His Asp Gln His Ala Arg Ser Ile
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<210> 187

<211> 2506

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1985)

<223>

<400> 187
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 actttgttaa agaaaaatca aatggctatg ttctatcaaa cggaataactt tcttaaaaaa 180
 cagcgattat ttccgtgacg acgactcaat taagatcgat gctgggaggc atgaatatga 240
 agagcacgta tgcttctgta tccagcaata cgaacgcttt tactctcagc ggtaaaggat 300
 tcggacacgg catcggtatg agtcagtacg gatcaaatgc cagagctgct gccgggacg 360
 attacaagaa gattttaagt ttctactatc caaatacgac tctatcaagc tattaataga 420
 gtttgaacag gaagcagcag tgccctcctt gttcatgttc aggggaaaac ataacattta 480
 catttttggg ggttattttt ttg aag gtc ttt ctt aaa gct gta cct atg ttg 533
 Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu
 1 5 10

tggtta cgg ttc ttt ttg ttt gtg cct aat gta ttt gcg gcc aac tct 581
 Trp Leu Arg Phe Phe Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser
 15 20 25

gtc aca aga ttg gac ggt gca aac cga tat gag gtt gcg gtg aac gtt 629
 Val Thr Arg Leu Asp Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val
 30 35 40

tcc aag cag ggg tgg aca agt gca agc act gtg att gtt gca aat gga 677
 Ser Lys Gln Gly Trp Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly
 45 50 55

aag gca tat gca gac gtc ctt tca gcg act cca ttt gcc tat cga aac 725
 Lys Ala Tyr Ala Asp Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn
 60 65 70 75

aac gcg cct gtt cta tta acg gaa gcg tct aaa ctg cca acg gcc act 773
 Asn Ala Pro Val Leu Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr
 80 85 90

aaa aac cga atc agt caa tta aaa cct agc aaa gtg atc gta atc ggc 821
 Lys Asn Arg Ile Ser Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly
 95 100

gga acc gtc agc gtt caa aac ggt gtc gta agc gag atc aaa aag ctt 869
 Gly Thr Val Ser Val Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu
 110 115 120

ggt gtg tca tct gtc gaa cgc atc ggc gga gcg aat cgc tac gag gtt 917
 Gly Val Ser Ser Val Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val
 125 130 135

gcg gcg aat att gcg aat aag ctg ccg agc aat tcg aaa gct gtc atc 965
 Ala Ala Asn Ile Ala Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile
 140 145 150 155

gca aac ggg acg gcc tat gct gac agc ctt gcg atc ggc gca tat gcc 1013
 Ala Asn Gly Thr Ala Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala
 160 165 170

gcg aga aac ggc atc ccg att ctt tta aca tcg tcg aat tcc ata ccg 1061
 Ala Arg Asn Gly Ile Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro
 175 180 185

aca gcg aca aaa aat gcg atg aag agc aaa gga aca aca tcg acc att 1109

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Thr	Ala	Thr	Lys	Asn	Ala	Met	Lys	Ser	Lys	Gly	Thr	Thr	Ser	Thr	Ile	
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gtc	gta	ggc	ggt	gaa	gtc	agc	atc	tcc	agc	agc	gtt	tac	aaa	cag	ctt	1157
Val	Val	Gly	Gly	Glu	Val	Ser	Ile	Ser	Ser	Ser	Val	Tyr	Lys	Gln	Leu	
	205					210					215					
gct	tct	ccg	acg	cgg	atc	ggc	ggc	agc	aac	cgc	tat	gaa	gtc	gcg	gcc	1205
Ala	Ser	Pro	Thr	Arg	Ile	Gly	Gly	Ser	Asn	Arg	Tyr	Glu	Val	Ala	Ala	
220					225					230					235	
aat	gtc	gtc	aag	aaa	tat	tat	tct	tct	gcc	aag	aat	gca	atc	atc	agc	1253
Asn	Val	Val	Lys	Lys	Tyr	Tyr	Ser	Ser	Ala	Lys	Asn	Ala	Ile	Ile	Ser	
				240					245					250		
aac	ggc	tat	gcg	tat	gcc	gac	gga	tta	aca	gga	tct	gtt	ctg	gcg	gct	1301
Asn	Gly	Tyr	Ala	Tyr	Ala	Asp	Gly	Leu	Thr	Gly	Ser	Val	Leu	Ala	Ala	
			255					260					265			
aag	caa	aac	cgt	ccg	atg	atg	ttc	acg	aat	gca	tca	tct	ttg	ccg	aca	1349
Lys	Gln	Asn	Arg	Pro	Met	Met	Phe	Thr	Asn	Ala	Ser	Ser	Leu	Pro	Thr	
		270					275					280				
ccg	aca	aga	gaa	gtg	atc	ggc	tcc	aaa	aac	atg	acg	acg	ttt	act	gtg	1397
Pro	Thr	Arg	Glu	Val	Ile	Gly	Ser	Lys	Asn	Met	Thr	Thr	Phe	Thr	Val	
	285					290					295					
ctt	ggc	gga	acg	gtt	tct	ctt	caa	tcc	aat	gtc	gtg	tca	cag	ctg	aag	1445
Leu	Gly	Gly	Thr	Val	Ser	Leu	Gln	Ser	Asn	Val	Val	Ser	Gln	Leu	Lys	
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aat	ccg	atc	gtc	ggc	aaa	aaa	atc	ttc	att	gat	gca	ggg	cac	gga	ggt	1493
Asn	Pro	Ile	Val	Gly	Lys	Lys	Ile	Phe	Ile	Asp	Ala	Gly	His	Gly	Gly	
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aca	gac	agc	ggt	gcc	ctc	ggc	aac	ggt	tta	tat	gag	aaa	agc	gtg	aac	1541
Thr	Asp	Ser	Gly	Ala	Leu	Gly	Asn	Gly	Leu	Tyr	Glu	Lys	Ser	Val	Asn	
			335					340					345			
ctt	gat	gtt	gca	aaa	tta	att	aat	acg	aaa	cta	tca	aac	ggc	ggt	gct	1589
Leu	Asp	Val	Ala	Lys	Leu	Ile	Asn	Thr	Lys	Leu	Ser	Asn	Gly	Gly	Ala	
		350					355					360				
ctg	cca	att	atg	gcg	aga	acg	aac	gac	act	tac	ctg	acg	ctc	gca	cag	1637
Leu	Pro	Ile	Met	Ala	Arg	Thr	Asn	Asp	Thr	Tyr	Leu	Thr	Leu	Ala	Gln	
	365					370					375					
cgc	gtg	tca	aaa	gcg	cag	tca	aat	cat	gcg	gat	ttg	ttt	gtc	agc	atc	1685
Arg	Val	Ser	Lys	Ala	Gln	Ser	Asn	His	Ala	Asp	Leu	Phe	Val	Ser	Ile	
380					385				390					395		
cat	gca	aac	tcg	gca	acg	cca	gct	gct	tcc	gga	aca	gaa	acc	tac	tat	1733
His	Ala	Asn	Ser	Ala	Thr	Pro	Ala	Ala	Ser	Gly	Thr	Glu	Thr	Tyr	Tyr	
				400					405					410		
tat	aca	aca	tat	gaa	tct	gcc	aac	agc	aaa	cgg	ctg	gca	acc	gag	att	1781
Tyr	Thr	Thr	Tyr	Glu	Ser	Ala	Asn	Ser	Lys	Arg	Leu	Ala	Thr	Glu	Ile	
			415					420					425			
caa	aac	cgt	ctc	tat	gtt	gca	ttg	aat	aca	aaa	aac	cgc	ggt	gta	aag	1829
Gln	Asn	Arg	Leu	Tyr	Val	Ala	Leu	Asn	Thr	Lys	Asn	Arg	Gly	Val	Lys	
		430					435					440				
atc	ggc	aac	ttc	cat	gtc	atc	agg	gaa	tca	aaa	atg	cca	agc	tgc	ctt	1877
Ile	Gly	Asn	Phe	His	Val	Ile	Arg	Glu	Ser	Lys	Met	Pro	Ser	Cys	Leu	
	445					450					455					
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 Ser Ser Thr Tyr Lys Glu Lys Gly Ala Lys Ala Ile Tyr Asp Gly Ile
 480 485 490
 gtt gct tac tat taaaatataa acagaaaact cgtttttcga aaaattgcct 2025
 Val Ala Tyr Tyr
 495
 atgctgcctt tgttttgtct ttattatata gtatgatatt tttggtgaaa ttaaagataa 2085
 aacggaggcg gtgcattttt aacaaaaaat caacgaattt actaatTTta ataactcctt 2145
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 cgagggtgtat gctagttagt atcgacaaaa gttaagaat gtacaatgaa tattcaagcc 2265
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 a 2506

<210> 188

<211> 495

<212> PRT

<213> Bacillus licheniformis

<400> 188

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Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val Ser Lys Gln Gly Trp
 35 40 45

Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly Lys Ala Tyr Ala Asp
 50 55 60

Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn Asn Ala Pro Val Leu
 65 70 75 80

Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr Lys Asn Arg Ile Ser
 85 90 95

Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly Gly Thr Val Ser Val
 100 105 110

Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu Gly Val Ser Ser Val
 115 120 125
 Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val Ala Ala Asn Ile Ala
 130 135 140
 Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile Ala Asn Gly Thr Ala
 145 150 155 160
 Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala Ala Arg Asn Gly Ile
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 Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro Thr Ala Thr Lys Asn
 180 185 190
 Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile Val Val Gly Gly Glu
 195 200 205
 Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu Ala Ser Pro Thr Arg
 210 215 220
 Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala Asn Val Val Lys Lys
 225 230 235 240
 Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser Asn Gly Tyr Ala Tyr
 245 250 255
 Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala Lys Gln Asn Arg Pro
 260 265 270
 Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr Pro Thr Arg Glu Val
 275 280 285
 Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val Leu Gly Gly Thr Val
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 Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys Asn Pro Ile Val Gly
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 Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly Thr Asp Ser Gly Ala
 325 330 335
 Leu Gly Asn Gly Leu Tyr Glu Lys Ser Val Asn Leu Asp Val Ala Lys
 340 345 350
 Leu Ile Asn Thr Lys Leu Ser Asn Gly Gly Ala Leu Pro Ile Met Ala
 355 360 365
 Arg Thr Asn Asp Thr Tyr Leu Thr Leu Ala Gln Arg Val Ser Lys Ala
 370 375 380

10294.000.ST25.txt

Gln Ser Asn His Ala Asp Leu Phe Val Ser Ile His Ala Asn Ser Ala
385 390 395 400

Thr Pro Ala Ala Ser Gly Thr Glu Thr Tyr Tyr Tyr Thr Thr Tyr Glu
405 410 415

Ser Ala Asn Ser Lys Arg Leu Ala Thr Glu Ile Gln Asn Arg Leu Tyr
420 425 430

Val Ala Leu Asn Thr Lys Asn Arg Gly Val Lys Ile Gly Asn Phe His
435 440 445

Val Ile Arg Glu Ser Lys Met Pro Ser Cys Leu Val Glu Leu Ala Phe
450 455 460

Ile Ser Asn Val Ser Asp Ala Thr Lys Leu Lys Ser Ser Thr Tyr Lys
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<210> 189

<211> 2110

<212> DNA

<213> Bacillus licheniformis

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<222> (501)..(1607)

<223>

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ctatatggga gagcgcgtca acatcatttc ctccggagat gaaacggcca gggaagtcag 180
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10294.000.ST25.txt
Met Leu Lys Lys Gly Met Lys Gly Ile Ala Val
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tca gat caa gcc tca gag gag ata gat ccg ccg cag gac atc aca tat Ser Asp Gln Ala 30 Ser Glu Glu 35 Ile Asp Pro Pro Gln Asp 40 Ile Thr Tyr	629
gta aaa gag gag aag gag caa gac aaa aca gac aaa acc aaa gat aaa Val Lys Glu Glu 45 Lys Glu Gln 50 Asp Lys Thr Asp Lys Thr Lys Asp Lys	677
aca gaa gac aaa ggc agc aaa acg aca agc gac gat aaa gcc gct caa Thr Glu Asp Lys Gly 60 Ser Lys Thr Thr Ser Asp Asp Lys Ala Ala Gln 75	725
acg ggc gat acg gtc atg aga gag ctt tat ctc att gat aag aac ggc Thr Gly Asp Thr 80 Val Met Arg Glu Leu Tyr 85 Ile Asp Lys Asn Gly 90	773
tat gtg aca gcg cag acg ctg ccg ctg cca aag cag gaa ggg acg gct Tyr Val Thr Ala 95 Gln Thr Leu Pro Leu 100 Pro Lys Gln Glu Gly 105 Thr Ala	821
aaa caa gcg ctt gaa tac ctc gtt gaa ggc ggc cct gtt tca aac atc Lys Gln Ala 110 Leu Glu Tyr Leu Val 115 Glu Gly Gly Pro Val Ser Asn Ile	869
ctg cca aac gga ttc aga gcc gtg ctg ccg gcg gat aca acg gtc aat Leu Pro 125 Asn Gly Phe Arg Ala 130 Val Leu Pro Ala Asp Thr Thr Val Asn	917
gtt gat att aaa gaa gac gga aca gcg atc gct gat ttc tca aat gaa Val Asp Ile Lys Glu Asp Gly Thr Ala 140 Ile Ala 150 Asp Phe Ser Asn Glu 155	965
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aca tgg acg tta acg cag ttt aac tcg att gat aaa gtg aag ctc cgc Thr Trp Thr Leu 175 Thr Gln Phe Asn Ser 180 Ile Asp Lys Val Lys Leu Arg 185	1061
atg aac ggc cat gat ttg aaa gaa atg cct gtt aac ggc acg ccg att Met Asn Gly His Asp Leu Lys 195 Glu Met Pro Val Asn Gly 200 Thr Pro Ile	1109
tca gaa gaa ctc agc cgc gag gac ggc att aac ctc gac acg gcg ggt Ser Glu Glu Leu Ser Arg Glu Asp Gly Ile Asn Leu 215 Asp Thr Ala Gly	1157
gtg aca gat ata acg gcg aca cag ccg gtc acc gtc tat tat ttg gct Val Thr Asp Ile Thr Ala 225 Thr Gln Pro Val Thr 230 Val Tyr Tyr Leu Ala 235	1205
gaa tca gat aaa ggc aca tat tac gtt ccg gtg aca aag cgg acg tct Glu Ser Asp Lys Gly Thr Tyr Tyr Val Pro Val Thr Lys Arg Thr Ser 250	1253
gca aaa gaa aaa gat cag gtg acg gcg gcg att aaa gag ctg act gaa Ala Lys Glu Lys 255 Asp Gln Val Thr Ala 260 Ala Ile Lys Glu Leu Thr Glu 265	1301
gga ccg gac aat aaa agc ggc ctg ctc tcc gat ttc cag ggc gac gtc	1349

10294.000.ST25.txt

Gly	Pro	Asp 270	Asn	Lys	Ser	Gly	Leu 275	Leu	Ser	Asp	Phe	Gln 280	Gly	Asp	Val		
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Lys	Leu 285	Glu	Asn	Lys	Pro	Lys 290	Ile	Glu	Asp	Gly	His 295	Val	Thr	Leu	Asp		
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Ser	Asp	Glu	Val	Leu 320	Asn	Ser	Ile	Val	Leu 325	Thr	Leu	Thr	Glu	Leu	Pro 330		
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Asp	Val	Lys	Ser 335	Val	Ser	Val	Thr	Val 340	Asn	Gly	Lys	Ser	Glu	Leu	Val 345		
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Asn	Glu	Lys 350	Gly	Glu	Lys	Leu	Ser 355	Lys	Pro	Val	Ser	Arg 360	Pro	Ser	Lys		
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			20					25					30				
Glu	Glu	Ile	Asp	Pro	Pro	Gln	Asp	Ile	Thr	Tyr	Val	Lys	Glu	Glu	Lys		
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Glu Gln Asp Lys Thr Asp Lys Thr Lys Asp Lys Thr Glu Asp Lys Gly
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 Ser Lys Thr Thr Ser Asp Asp Lys Ala Ala Gln Thr Gly Asp Thr Val
 65 70 75 80
 Met Arg Glu Leu Tyr Leu Ile Asp Lys Asn Gly Tyr Val Thr Ala Gln
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 Thr Leu Pro Leu Pro Lys Gln Glu Gly Thr Ala Lys Gln Ala Leu Glu
 100 105 110
 Tyr Leu Val Glu Gly Gly Pro Val Ser Asn Ile Leu Pro Asn Gly Phe
 115 120 125
 Arg Ala Val Leu Pro Ala Asp Thr Thr Val Asn Val Asp Ile Lys Glu
 130 135 140
 Asp Gly Thr Ala Ile Ala Asp Phe Ser Asn Glu Phe Lys Asn Tyr Lys
 145 150 155 160
 Ala Glu Asp Glu Gln Lys Ile Val Gln Ala Ile Thr Trp Thr Leu Thr
 165 170 175
 Gln Phe Asn Ser Ile Asp Lys Val Lys Leu Arg Met Asn Gly His Asp
 180 185 190
 Leu Lys Glu Met Pro Val Asn Gly Thr Pro Ile Ser Glu Glu Leu Ser
 195 200 205
 Arg Glu Asp Gly Ile Asn Leu Asp Thr Ala Gly Val Thr Asp Ile Thr
 210 215 220
 Ala Thr Gln Pro Val Thr Val Tyr Tyr Leu Ala Glu Ser Asp Lys Gly
 225 230 235 240
 Thr Tyr Tyr Val Pro Val Thr Lys Arg Thr Ser Ala Lys Glu Lys Asp
 245 250 255
 Gln Val Thr Ala Ala Ile Lys Glu Leu Thr Glu Gly Pro Asp Asn Lys
 260 265 270
 Ser Gly Leu Leu Ser Asp Phe Gln Gly Asp Val Lys Leu Glu Asn Lys
 275 280 285
 Pro Lys Ile Glu Asp Gly His Val Thr Leu Asp Phe Asn Glu Ala Ile
 290 295 300
 Tyr Gly Ser Ala Asp Gly Gln Lys Lys Val Ile Ser Asp Glu Val Leu
 305 310 315 320

Asn Ser Ile Val Leu Thr Leu Thr Glu Leu Pro Asp Val Lys Ser Val
 325 330 335

Ser Val Thr Val Asn Gly Lys Ser Glu Leu Val Asn Glu Lys Gly Glu
 340 345 350

Lys Leu Ser Lys Pro Val Ser Arg Pro Ser Lys Val Asn Thr Gly Ser
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Phe

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<211> 2169

<212> DNA

<213> Bacillus licheniformis

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<221> CDS

<222> (501)..(1667)

<223>

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gaatttcttt ttttatatgg gaacacggac aaaatggact ctattttaaa cattctgatc 180

tggtgttttt ggaagcaaaa tgctttcaca taaccgtttt ttatttcttt cacaagaatc 240

gccccgttag aaaaaccgct ttttttcatt tatatgattt ctaccggaat gccgtcttcc 300

atggaacgat acaacagctt attcatcgct tcacctcaca ttctatttta tacgaacatt 360

tggtcttgat caagtgtaaa caaaatgtaa attttggcat tattcgagtt catgtatgaa 420

aatattagca ttttgaagaa actttttaag gggttattgc gtcagtaa acgtcacata 480

taaaagaagg agtaccgcgac atg gca aga aca tac aga acg cga ata aag aaa 533
 Met Ala Arg Thr Tyr Arg Thr Arg Ile Lys Lys
 1 5 10

aga aaa aag cag aaa aca aaa aga agg ctt atc ata ttt tcc ttt ttg 581
 Arg Lys Lys Gln Lys Thr Lys Arg Arg Leu Ile Ile Phe Ser Phe Leu
 15 20 25

gtt gtt tgt gga tta att tat ctt gca ctt cca agc ggt atg cga gat 629
 Val Val Cys Gly Leu Ile Tyr Leu Ala Leu Pro Ser Gly Met Arg Asp
 30 35 40

cac cag gaa aac caa ttg caa gca act gaa aaa aag gca cag cct gaa 677
 His Gln Glu Asn Gln Leu Gln Ala Thr Glu Lys Lys Ala Gln Pro Glu
 45 50 55

10294.000.ST25.txt

gca aag aaa aag cca aca caa aat gaa aca aaa aag agc aaa atc gtc Ala Lys Lys Lys Pro Thr Gln Asn Glu Thr Lys Lys Ser Lys Ile Val 60 65 70 75	725
aca aaa aat gat aat gct caa ttg gat caa tat ttg aaa agc att gga Thr Lys Asn Asp Asn Ala Gln Leu Asp Gln Tyr Leu Lys Ser Ile Gly 80 85 90	773
ttc agc ggc aca gca ttg atc gta gaa gat gga aaa gtg gtg aca agc Phe Ser Gly Thr Ala Leu Ile Val Glu Asp Gly Lys Val Val Thr Ser 95 100 105	821
aaa ggg tat tta tat gca aac cgc gag gaa atg gtt ccc aat aca cca Lys Gly Tyr Leu Tyr Ala Asn Arg Glu Glu Met Val Pro Asn Thr Pro 110 115 120	869
gat acc gtc ttt tat gtg ggg tca tca caa aaa gcg att att gca acg Asp Thr Val Phe Tyr Val Gly Ser Ser Gln Lys Ala Ile Ile Ala Thr 125 130 135	917
gca att tta cag ctg gag gaa aaa gga ttg cta tct gta aat gac cct Ala Ile Leu Gln Leu Glu Glu Lys Gly Leu Leu Ser Val Asn Asp Pro 140 145 150 155	965
gtt tct aag tat ctt ccc aat ttt cca aac ggc tca aag atc acc ctt Val Ser Lys Tyr Leu Pro Asn Phe Pro Asn Gly Ser Lys Ile Thr Leu 160 165 170	1013
tat cat ttc ttg acg cac aca tcc gga att agg ggt cac aaa gaa ggc Tyr His Phe Leu Thr His Thr Ser Gly Ile Arg Gly His Lys Glu Gly 175 180 185	1061
cgc gga tat att tcg ccg gaa gat tta att aaa gat atc gaa aaa cgg Arg Gly Tyr Ile Ser Pro Glu Asp Leu Ile Lys Asp Ile Glu Lys Arg 190 195 200	1109
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caa tac atc aaa aag cat att ttt aaa cct gcc ggt atg aaa cat gca Gln Tyr Ile Lys Lys His Ile Phe Lys Pro Ala Gly Met Lys His Ala 240 245 250	1253
ggc ttt tat aaa aca ttt gct aaa gag tca aat cca tcg aca gga tat Gly Phe Tyr Lys Thr Phe Ala Lys Glu Ser Asn Pro Ser Thr Gly Tyr 255 260 265	1301
aaa tta aac ctg caa aaa aag ctt tat acg cct gac atg ccg gat tta Lys Leu Asn Leu Gln Lys Lys Leu Tyr Thr Pro Asp Met Pro Asp Leu 270 275 280	1349
tca cag ctt tac ggg gcc ggt gat att tat atg acc gct tat gac atg Ser Gln Leu Tyr Gly Ala Gly Asp Ile Tyr Met Thr Ala Tyr Asp Met 285 290 295	1397
tat ttg ttt gat aaa gca ctt tac gaa aga aaa atc att tcc aat gaa Tyr Leu Phe Asp Lys Ala Leu Tyr Glu Arg Lys Ile Ile Ser Asn Glu 300 305 310 315	1445
agt ttt atg aaa atg ttt acg ccg aat aaa gca aca tac ggc atg ggc Ser Phe Met Lys Met Phe Thr Pro Asn Lys Ala Thr Tyr Gly Met Gly 320 325 330	1493

10294.000.ST25.txt

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ttt tat gtg tct cca gga agc tat tca agc cac ggt gtc atg ccc ggc 1541
Phe Tyr Val Ser Pro Gly Ser Tyr Ser Ser His Gly Val Met Pro Gly
335 340 345

tac aac ata tta aac agt ttc agt ctg aca ggg agc aga tac gtc att 1589
Tyr Asn Ile Leu Asn Ser Phe Ser Leu Thr Gly Ser Arg Tyr Val Ile
350 355 360

cta ttt tca aac atc caa aac aac att aag tct ttt ggc agt gtg aat 1637
Leu Phe Ser Asn Ile Gln Asn Asn Ile Lys Ser Phe Gly Ser Val Asn
365 370 375

aat cgg atc ttc tct att tta aat gga ttt tgaacagcag agaaagtttt 1687
Asn Arg Ile Phe Ser Ile Leu Asn Gly Phe
380 385

tacagctaaa agggatttta attataaatg tagaagatag atgataaatg aattttcaat 1747
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gttgctgcat tatttatatg gactttttaa gactcaaaac agcatgaacc tgatacgta 1867
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<211> 389

<212> PRT

<213> Bacillus licheniformis

<400> 192

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Thr Lys Arg Arg Leu Ile Ile Phe Ser Phe Leu Val Val Cys Gly Leu
20 25 30

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Ile Tyr Leu Ala Leu Pro Ser Gly Met Arg Asp His Gln Glu Asn Gln
35 40 45

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Leu Gln Ala Thr Glu Lys Lys Ala Gln Pro Glu Ala Lys Lys Lys Pro
50 55 60

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Thr Gln Asn Glu Thr Lys Lys Ser Lys Ile Val Thr Lys Asn Asp Asn
65 70 75 80

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Ala Gln Leu Asp Gln Tyr Leu Lys Ser Ile Gly Phe Ser Gly Thr Ala
 85 90

Leu Ile Val Glu Asp Gly Lys Val Val Thr Ser Lys Gly Tyr Leu Tyr
 100 105 110

Ala Asn Arg Glu Glu Met Val Pro Asn Thr Pro Asp Thr Val Phe Tyr
 115 120 125

Val Gly Ser Ser Gln Lys Ala Ile Ile Ala Thr Ala Ile Leu Gln Leu
 130 135 140

Glu Glu Lys Gly Leu Leu Ser Val Asn Asp Pro Val Ser Lys Tyr Leu
 145 150 155 160

Pro Asn Phe Pro Asn Gly Ser Lys Ile Thr Leu Tyr His Phe Leu Thr
 165 170 175

His Thr Ser Gly Ile Arg Gly His Lys Glu Gly Arg Gly Tyr Ile Ser
 180 185 190

Pro Glu Asp Leu Ile Lys Asp Ile Glu Lys Arg Gly Val Lys Tyr Pro
 195 200 205

Thr Gly Lys Trp Asp Tyr Arg Asp Ser Asn Tyr Ser Val Leu Ala Tyr
 210 215 220

Ile Val Ser Met Val Ser Gly Glu Pro Val Asp Gln Tyr Ile Lys Lys
 225 230 235 240

His Ile Phe Lys Pro Ala Gly Met Lys His Ala Gly Phe Tyr Lys Thr
 245 250 255

Phe Ala Lys Glu Ser Asn Pro Ser Thr Gly Tyr Lys Leu Asn Leu Gln
 260 265 270

Lys Lys Leu Tyr Thr Pro Asp Met Pro Asp Leu Ser Gln Leu Tyr Gly
 275 280 285

Ala Gly Asp Ile Tyr Met Thr Ala Tyr Asp Met Tyr Leu Phe Asp Lys
 290 295 300

Ala Leu Tyr Glu Arg Lys Ile Ile Ser Asn Glu Ser Phe Met Lys Met
 305 310 315 320

Phe Thr Pro Asn Lys Ala Thr Tyr Gly Met Gly Phe Tyr Val Ser Pro
 325 330 335

Gly Ser Tyr Ser Ser His Gly Val Met Pro Gly Tyr Asn Ile Leu Asn
 340 345 350

Ser Phe Ser Leu Thr Gly Ser Arg Tyr Val Ile Leu Phe Ser Asn Ile
 355 360 365

Gln Asn Asn Ile Lys Ser Phe Gly Ser Val Asn Asn Arg Ile Phe Ser
 370 375 380

Ile Leu Asn Gly Phe
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<210> 193

<211> 1492

<212> DNA

<213> Bacillus licheniformis

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<221> CDS

<222> (501)..(989)

<223>

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 gctcaatgct gcgatgatca gcgttttaac gggccagccg cttcgtttca attgaccgcg 180
 gaaagccgcg aacaagagca gggatgatgcc gccgacagcc attctgacag cgccgaacac 240
 aagaggtgcc gcctcttttcg gcgcaaatgc ctgggttggc cccgtcgttc cccataaaat 300
 tgccgcaagc aagacaaaca gaaccgatac tttcatacta acgatctctc cctactcgat 360
 cattcagaac tttttctatt gtaagataag tttgcggatt tttgaatcgc cgcttcggaa 420
 atttccctga aaagaggaaa tattcaacgc tggccgaatt catataatgg ccaaaaaaca 480
 attaaagtcg gaggaagcgg atg aaa aaa cga aca gtt tta ttc ttc ttg ttg 533
 Met Lys Lys Arg Thr Val Leu Phe Phe Leu Leu
 1 5 10
 atc tgg ctc gcc gga tgt gcg agc gcc caa gag gct gag gaa caa acc 581
 Ile Trp Leu Ala Gly Cys Ala Ser Ala Gln Glu Ala Glu Glu Gln Thr
 15 20 25
 aaa tgg gtg aac agc gaa cag aaa gcg att gag aac ggc att cgt tat 629
 Lys Trp Val Asn Ser Glu Gln Lys Ala Ile Glu Asn Gly Ile Arg Tyr
 30 35 40
 gaa agc att aca aaa gac gat att ata gac aaa atc gat tta aac ggt 677
 Glu Ser Ile Thr Lys Asp Asp Ile Ile Asp Lys Ile Asp Leu Asn Gly
 45 50 55
 gaa caa gtc gtc gtt ttt cga ttc ggc gat tcg gag gga gag ggg att 725
 Glu Gln Val Val Val Phe Arg Phe Gly Asp Ser Glu Gly Glu Gly Ile
 60 65 70 75

10294.000.ST25.txt

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ggc ctc gca cac atc aaa agg gaa aac ggc aac tat caa tgg tac cgc      773
Gly Leu Ala His Ile Lys Arg Glu Asn Gly Asn Tyr Gln Trp Tyr Arg
80 85 90

gac tta aat tac gca att gta aaa tcg gac cac ccg aaa acg gag aat      821
Asp Leu Asn Tyr Ala Ile Val Lys Ser Asp His Pro Lys Thr Glu Asn
95 100 105

gcg gaa gct tcc gcg ccg ttc aca acc cct aag gga aga aag tac acg      869
Ala Glu Ala Ser Ala Pro Phe Thr Thr Pro Lys Gly Arg Lys Tyr Thr
110 115 120

tta tat aca ggg gat gca gat cgc ctg aat ggt aca ttt gag act gat      917
Leu Tyr Thr Gly Asp Ala Asp Arg Leu Asn Gly Thr Phe Glu Thr Asp
125 130 135

gac ggg ctt cat ttg gag ccg gtg gtc gat caa aaa acg ggc atg tat      965
Asp Gly Leu His Leu Glu Pro Val Val Asp Gln Lys Thr Gly Met Tyr
140 145 150 155

tat cag atc gtg cag gat tcg gac tgaaatgaaa caaaaatgct gtcgggttgt      1019
Tyr Gln Ile Val Gln Asp Ser Asp
160

tcccgacagc atttcatttt ttacgatttc tttttccgca ctgtcaagag cagcgcagca      1079

cctccaagaa gcacggcgag gatcgacagg atcagggaag cggtttgaat cccttgcct      1139

ccttgactgt cttcattttc tgcggcagcg ttttgtttcg ttgaagcgcc gtgtgcatca      1199

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gcgtcatcat caccgggtcca ctgcacaatt gtgccgtcct tataatattg gtatgcgttc      1319

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<210> 194

<211> 163

<212> PRT

<213> Bacillus licheniformis

<400> 194

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Glu Gln Lys Ala Ile Glu Asn Gly Ile Arg Tyr Glu Ser Ile Thr Lys
35 40 45

Asp Asp Ile Ile Asp Lys Ile Asp Leu Asn Gly Glu Gln Val Val Val
50 55 60

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10294.000.ST25.txt

Phe Arg Phe Gly Asp Ser Glu Gly Glu Gly Ile Gly Leu Ala His Ile
65 70 75 80

Lys Arg Glu Asn Gly Asn Tyr Gln Trp Tyr Arg Asp Leu Asn Tyr Ala
85 90 95

Ile Val Lys Ser Asp His Pro Lys Thr Glu Asn Ala Glu Ala Ser Ala
100 105 110

Pro Phe Thr Thr Pro Lys Gly Arg Lys Tyr Thr Leu Tyr Thr Gly Asp
115 120 125

Ala Asp Arg Leu Asn Gly Thr Phe Glu Thr Asp Asp Gly Leu His Leu
130 135 140

Glu Pro Val Val Asp Gln Lys Thr Gly Met Tyr Tyr Gln Ile Val Gln
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Asp Ser Asp

<210> 195

<211> 1988

<212> DNA

<213> Bacillus licheniformis

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<221> CDS

<222> (501)..(1490)

<223>

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cgaccaacag ggggatgaag atg aag aag ctg tta gtt gtt tat gcc gtg atg 533

10294.000.ST25.txt
Met Lys Lys Leu Leu Val Val Tyr Ala Val Met
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ctc tgt ttg ttt ttt ctg tat gtc tac gac tac tcc cgg ggc gat aaa	581
Leu Cys Leu Phe Phe Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys	
	15 20 25
gcc ggt tct gca gaa gaa agc agg agg cct gcg gcc gca ggc agt ctg	629
Ala Gly Ser Ala Glu Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu	
	30 35 40
tcc gaa aaa tac gtg atg gtc acg ttt caa tcg gga atc gaa tat tgg	677
Ser Glu Lys Tyr Val Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp	
	45 50 55
aag agc ggt ctg aaa ggc ttt gag gat gcc gcg cag ctt ttc aac gtc	725
Lys Ser Gly Leu Lys Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val	
	60 65 70 75
tct gtc gag tat cgg ggg gcg gcc cat tat gat gtc cat gag caa acg	773
Ser Val Glu Tyr Arg Gly Ala Ala His Tyr Asp Val His Glu Gln Thr	
	80 85 90
acc gtc ctc gag cag gtg att gca aaa aaa ccg gcg gga atc gct gtt	821
Thr Val Leu Glu Gln Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val	
	95 100 105
tcg gca ata aac cca aaa gct tta aac cct gtc atc gac aag gcg cac	869
Ser Ala Ile Asn Pro Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His	
	110 115 120
gag cag ggt att ccg atc gtt tta ttt gat tca gac gcc ccg ctc agc	917
Glu Gln Gly Ile Pro Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser	
	125 130 135
aaa gct tct aca tat atc ggc aca aat aat atg gaa gcg ggt gct gtg	965
Lys Ala Ser Thr Tyr Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val	
	140 145 150 155
gcc gca agg cga atg gcc gaa ttt ttg aat gga aag gga gaa acc gcg	1013
Ala Ala Arg Arg Met Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala	
	160 165 170
gtc att acc cag ccg cag cag tac aat cat cag gaa agg acg aag ggc	1061
Val Ile Thr Gln Pro Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly	
	175 180 185
ttt gaa caa acg atc aag caa aaa tac ccg aac atg aag gtt gcc gcg	1109
Phe Glu Gln Thr Ile Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala	
	190 195 200
gtt ttg gac gga aaa ggg gat gag ctg acg tcg aaa aaa gaa gcg gcg	1157
Val Leu Asp Gly Lys Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala	
	205 210 215
aag att ttg gag gaa aat ccg tcc atc aaa gga att ttc acg act gaa	1205
Lys Ile Leu Glu Glu Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu	
	220 225 230 235
gcc aat gga gcg agc ggc gtg gcc cgt gct gtg aag gag gcg gga ctt	1253
Ala Asn Gly Ala Ser Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu	
	240 245 250
gaa ggg gaa gta tgt atc atc ggc ttt gat aaa gac aag aaa acg ctg	1301
Glu Gly Glu Val Cys Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu	
	255 260 265
gac ggc atc aaa aac gga tcg att tcc gcg aca atg agc cag gac aca	1349

10294.000.ST25.txt

Asp Gly Ile Lys Asn Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr
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 Trp Gln Met Gly Tyr Trp Ser Leu His Met Leu Phe Phe Ser Asn His
 285 290 295
 cat ctg aag cat gaa cgc ccg ctt ccg gcc gca atc gac aca ggc att 1445
 His Leu Lys His Glu Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile
 300 305 310 315
 acc atc ata acg aaa gaa aat gtg gca gcc tat tat gcg aat gat 1490
 Thr Ile Ile Thr Lys Glu Asn Val Ala Ala Tyr Tyr Ala Asn Asp
 320 325 330
 taaacgtttg atcaataatg cgccgatccg tcataagctg atcagccttc tcttgtaaat 1550
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 gcagggcctg acttctttat attccgaagc agcgggtatt ctcgttgtca atgataaggg 1850
 tgagatgatc agcaatgaga tgtatgaacg cacgccgaca gatttgacaa aagaaccatg 1910
 gtatcaggcg gctctcgaca atgaagggat tttcaagatg atcgggaagc ctgtcaaccg 1970
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<210> 196

<211> 330

<212> PRT

<213> Bacillus licheniformis

<400> 196

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 Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu Ser Glu Lys Tyr Val
 35 40 45
 Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp Lys Ser Gly Leu Lys
 50 55 60
 Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val Ser Val Glu Tyr Arg
 65 70 75 80
 Gly Ala Ala His Tyr Asp Val His Glu Gln Thr Thr Val Leu Glu Gln
 85 90 95

Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val Ser Ala Ile Asn Pro
 100 105 110
 Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His Glu Gln Gly Ile Pro
 115 120 125
 Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser Lys Ala Ser Thr Tyr
 130 135 140
 Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val Ala Ala Arg Arg Met
 145 150 155 160
 Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala Val Ile Thr Gln Pro
 165 170 175
 Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly Phe Glu Gln Thr Ile
 180 185 190
 Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala Val Leu Asp Gly Lys
 195 200 205
 Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala Lys Ile Leu Glu Glu
 210 215 220
 Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu Ala Asn Gly Ala Ser
 225 230 235 240
 Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu Glu Gly Glu Val Cys
 245 250 255
 Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu Asp Gly Ile Lys Asn
 260 265 270
 Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr Trp Gln Met Gly Tyr
 275 280 285
 Trp Ser Leu His Met Leu Phe Phe Ser Asn His His Leu Lys His Glu
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<211> 1677

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1190)

<223>

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 cattggccaa ccttttaacg cagctatcgc ccgaatgtgt atcggataca tgataaccca 180
 gcgtaaagat aggaaggggc gagtgcgggg ggggggggctg gggggggccg gggggggcgtc 240
 ggtggggggg gacagggcag gggcagttgg tagcgcgtgg tggaggtggg ccggggccga 300
 tgtggggggg gcgcgctgtc gggggcaatg cgtcattgta agtgagtga tttggttgcg 360
 ggggcaggat ttgagcctgg gacttcgggt tatagccgga cgagctgccg aactgcacca 420
 ggctgttgag taccaggggt gtatgaaatg ttcagccctt ttgcccaata agaaaaaata 480
 aaactgggag cgagaagatg atg aaa cga atc tgt gcc ata tgc tgg gga tcc 533
 Met Lys Arg Ile Cys Ala Ile Cys Trp Gly Ser
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 Leu Leu Thr Leu Ala Phe Ser Gly Asn Ala Glu Ala Ile Ser Asn Lys
 15 20 25
 gcg atc cat tgg ggt ttt tca aaa agc aaa aac cat cag ccg gca gat 629
 Ala Ile His Trp Gly Phe Ser Lys Ser Lys Asn His Gln Pro Ala Asp
 30 35 40
 gcg ggt caa gag ctg acc aac ctt tta cag cag tac gac gcc ttt tat 677
 Ala Gly Gln Glu Leu Thr Asn Leu Leu Gln Gln Tyr Asp Ala Phe Tyr
 45 50 55
 ttg ggc aac aca aag gaa aaa acg atc tat ctg acc ttt gat aac ggc 725
 Leu Gly Asn Thr Lys Glu Lys Thr Ile Tyr Leu Thr Phe Asp Asn Gly
 60 65 70 75
 tat gaa aac ggc tac acc cct cag gtg ctc gat gtt ctg aaa aaa caa 773
 Tyr Glu Asn Gly Tyr Thr Pro Gln Val Leu Asp Val Leu Lys Lys Gln
 80 85 90
 aac gtc aaa gcg gcc ttt ttt gtg acg ggc cat ttt gtc aaa gat cag 821
 Asn Val Lys Ala Ala Phe Phe Val Thr Gly His Phe Val Lys Asp Gln
 95 100 105
 ccg gag ctg atc aag cga atg gcc gag gag ggg cat atc atc ggg aat 869
 Pro Glu Leu Ile Lys Arg Met Ala Glu Glu Gly His Ile Ile Gly Asn
 110 115 120
 cat tca tat cac cat ccg gat ctg acg acg aaa aca agc cgc gtc att 917
 His Ser Tyr His His Pro Asp Leu Thr Thr Lys Thr Ser Arg Val Ile
 125 130 135
 caa gag gaa ttg gaa tcg gtc gat gag gag gtt tac aaa atc aca ggc 965

10294.000.ST25.txt

Gln Glu Glu Leu Glu Ser Val Asp Glu Glu Val Tyr Lys Ile Thr Gly
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 Glu Lys Asn Asn Leu Tyr Leu Arg Pro Pro Arg Gly Ile Phe Ser Glu
 160 165 170
 cgg gtg ctc gaa gaa acg aaa aag ctc ggc tat caa acg gta ttc tgg 1061
 Arg Val Leu Glu Glu Thr Lys Lys Leu Gly Tyr Gln Thr Val Phe Trp
 175 180 185
 tct gtt gct ttt gtc gat tgg aaa atc aat gcc caa aaa ggg tgg cgc 1109
 Ser Val Ala Phe Val Asp Trp Lys Ile Asn Ala Gln Lys Gly Trp Arg
 190 195 200
 tat gcg tac gac aat atg atg aaa cag gct cac ccc ggc gcc atc tat 1157
 Tyr Ala Tyr Asp Asn Met Met Lys Gln Ala His Pro Gly Ala Ile Tyr
 205 210 215
 ctg ctt cac acc gtc ttc agg cga tca ccg act tgaaaaaaga aggttataca 1210
 Leu Leu His Thr Val Phe Arg Arg Ser Pro Thr
 220 225 230
 tttaaaagcc tcgatgacct gatgtttgaa aaatctatga tgcttgagac ccttgaaaga 1270
 acaatgcccc ggtgccgagg tcgcaatgcg taaaacattt gtttttcccc cccccaaga 1330
 ccccgctctca aataatataa aatagatata aaaaaaaga atcataataa aaaaagaata 1390
 tctatcccca ccaaagggag ggtggttttg ataaccagtc gcagtcgggg gaaagtgctc 1450
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 <212> PRT
 <213> *Bacillus licheniformis*

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 35 40 45
 Thr Asn Leu Leu Gln Gln Tyr Asp Ala Phe Tyr Leu Gly Asn Thr Lys
 50 55 60

Glu Lys Thr Ile Tyr Leu Thr Phe Asp Asn Gly Tyr Glu Asn Gly Tyr
65 70 75 80

Thr Pro Gln Val Leu Asp Val Leu Lys Lys Gln Asn Val Lys Ala Ala
85 90 95

Phe Phe Val Thr Gly His Phe Val Lys Asp Gln Pro Glu Leu Ile Lys
100 105 110

Arg Met Ala Glu Glu Gly His Ile Ile Gly Asn His Ser Tyr His His
115 120 125

Pro Asp Leu Thr Thr Lys Thr Ser Arg Val Ile Gln Glu Glu Leu Glu
130 135 140

Ser Val Asp Glu Glu Val Tyr Lys Ile Thr Gly Glu Lys Asn Asn Leu
145 150 155 160

Tyr Leu Arg Pro Pro Arg Gly Ile Phe Ser Glu Arg Val Leu Glu Glu
165 170 175

Thr Lys Lys Leu Gly Tyr Gln Thr Val Phe Trp Ser Val Ala Phe Val
180 185 190

Asp Trp Lys Ile Asn Ala Gln Lys Gly Trp Arg Tyr Ala Tyr Asp Asn
195 200 205

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225 230

<210> 199

<211> 4041

<212> DNA

<213> Bacillus licheniformis

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<221> CDS

<222> (501)..(3641)

<223>

<400> 199

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cttttcataa agtattttca gtccacacca tttatttttg gacggatttc aaacaggcat 120

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tcaagcaact gcttgaggaa agccatttca gagacatcac ggtacatatg aacaaaaatt	300
actgctgcat ttctgcggta aaatcatgaa ctttgtatga tcatcccttt caatacggaa	360
gggatttttt atgtttgata gagttgaaac tggatcttaa atatcatatt tttgattttt	420
aaagaaaagt attccattaa catagcaaac atgggttaat atcaaagtga acgtttttac	480
tatatatttcc ggagggtattt atg aac aaa agg atc gtg aaa agt tca att gtt	533
Met Asn Lys Arg Ile Val Lys Ser Ser Ile Val	
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ttc ttt ctc ctt gcc gca tta att ttt ggc cag ctg cct tta ccg aag	581
Phe Phe Leu Leu Ala Ala Leu Ile Phe Gly Gln Leu Pro Leu Pro Lys	
15 20 25	
aca atg gca gcg gaa gac agc gtt ccg aat aac gaa acc aca ttg acc	629
Thr Met Ala Ala Glu Asp Ser Val Pro Asn Asn Glu Thr Thr Leu Thr	
30 35 40	
agc gcg tcc cct gtt gaa gct tcg ttt caa agc gat gac gag gtg cat	677
Ser Ala Ser Pro Val Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His	
45 50 55	
tgg tat aaa gtc aat cct tca aat cag gaa atc gca aac tat acg cac	725
Trp Tyr Lys Val Asn Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His	
60 65 70 75	
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Phe Arg Val Lys Leu Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr	
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Ser Ser Leu Glu Asn Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn	
95 100 105	
ggc tac tcc tat gaa aat aat cct gct tta atc gat ttt ccg att gcc	869
Gly Tyr Ser Tyr Glu Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala	
110 115 120	
tgg aaa ggt cct tac tac ata aaa gta gaa aat cac cat gat gag gaa	917
Trp Lys Gly Pro Tyr Tyr Ile Lys Val Glu Asn His His Asp Glu Glu	
125 130 135	
aac gaa acc act tca att aca gat att tct tac acc atc agc tat gaa	965
Asn Glu Thr Thr Ser Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu	
140 145 150 155	
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Gly Val Thr Leu Pro Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro	
160 165 170	
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Ala Glu Leu Ser Val Ser Glu Arg Glu Thr Gly Lys Gly Ile Leu Lys	
175 180 185	
cag tta aga acg atc agg gat gaa gtt ctt tca aaa act gaa aaa gga	1109
Gln Leu Arg Thr Ile Arg Asp Glu Val Leu Ser Lys Thr Glu Lys Gly	
190 195 200	
aaa gag ctg tct tcc ctt tac tat aaa gca gct cca ttc atc agc gca	1157
Lys Glu Leu Ser Ser Leu Tyr Tyr Lys Ala Ala Pro Phe Ile Ser Ala	
205 210 215	

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gtg Val	cag Gln	ctg Leu	aag Lys	ccg Pro 240	ctg Leu	ttt Phe	gca Ala	gat Asp	gtc Val 245	gct Ala	aaa Lys	aac Asn	gga Gly	caa Gln 250	gtg Val	1253
agc Ser	gca Ala	tac Tyr	tcg Ser 255	att Ile	acg Thr	aat Asn	gat Asp	gat Asp 260	caa Gln	aaa Lys	gcg Ala	atc Ile	agt Ser 265	cgc Arg	ctg Leu	1301
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gat Asp	caa Gln 285	gtc Val	gcg Ala	aaa Lys	gac Asp	atc Ile 290	ggc Gly	atc Ile	gaa Glu	caa Gln	tta Leu 295	aca Thr	ggc Gly	agc Ser	aaa Lys	1397
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gcg Ala	ccc Pro	gaa Glu	aac Asn	cgt Arg 320	tac Tyr	atc Ile	gta Val	aaa Lys	ttg Leu 325	aaa Lys	gaa Glu	ggc Gly	aaa Lys	aaa Lys 330	ccg Pro	1493
gga Gly	tct Ser	ttc Phe	aaa Lys 335	tct Ser	aaa Lys	gcc Ala	caa Gln	tca Ser 340	tcc Ser	ggc Gly	gtc Val	cag Gln	gca Ala 345	tta Leu	gag Glu	1541
ccc Pro	ctc Leu	ggt Gly 350	aaa Lys	agc Ser	aaa Lys	acg Thr	gca Ala 355	ttt Phe	aaa Lys	gat Asp	atg Met	tac Tyr 360	gtt Val	gtg Val	gaa Glu	1589
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cag Gln 380	gcg Ala	gca Ala	gcc Ala	tcc Ser	aag Lys 385	atc Ile	gcc Ala	aag Lys	atg Met	cct Pro 390	gaa Glu	gtg Val	gaa Glu	ttc Phe	gtc Val 395	1685
gaa Glu	cag Gln	gtt Val	cag Gln	caa Gln 400	tat Tyr	gaa Glu	gca Ala	ctg Leu	tca Ser 405	aga Arg	gac Asp	acc Thr	caa Gln	tat Tyr 410	cca Pro	1733
tat Tyr	caa Gln	tgg Trp	tcg Ser 415	ctc Leu	aaa Lys	aat Asn	aac Asn	ggc Gly 420	aaa Lys	aac Asn	cgt Arg	gct Ala	gcg Ala 425	aat Asn	gct Ala	1781
gac Asp	ata Ile	caa Gln 430	ttt Phe	gaa Glu	cag Gln	ctt Leu	cag Gln 435	aag Lys	ctg Leu	atg Met	aaa Lys	ggc Gly 440	aaa Lys	aag Lys	ctg Leu	1829
aaa Lys	gat Asp 445	aca Thr	gta Val	atc Ile	gcc Ala	gtc Val 450	gtt Val	gac Asp	aca Thr	ggc Gly	gtt Val 455	gat Asp	cat His	acc Thr	ctt Leu	1877
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ggc Gly	cgc Arg	acg Thr	gcg Ala	gat Asp 480	gcg Ala	atg Met	gat Asp	gac Asp	aat Asn 485	ggc Gly	cac His	ggc Gly	aca Thr	cac His 490	gtg Val	1973

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ggc Gly	agt Ser 525	gga Gly	gat Asp	acg Thr	gaa Glu	cag Gln 530	att Ile	gca Ala	aac Asn	ggc Gly	atc Ile 535	atc Ile	tat Tyr	gcc Ala	gcc Ala	2117
gac Asp 540	cac His	ggt Gly	gca Ala	aaa Lys	gtc Val 545	atc Ile	aat Asn	tta Leu	agt Ser	ctt Leu 550	ggc Gly	ggg Gly	cca Pro	tac Tyr	agc Ser 555	2165
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cca Pro	aac Asn 685	ccg Pro	gat Asp	tat Tyr	gac Asp	ctg Leu 690	gat Asp	ata Ile	gaa Glu	ccg Pro	gct Ala 695	gca Ala	caa Gln	att Ile	ccc Pro	2597
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gcc Ala	agc Ser	gtt Val	ttt Phe	gag Glu 720	ctg Leu	aac Asn	atg Met	aag Lys	gtt Val 725	cat His	ccc Pro	gtt Val	tta Leu	aac Asn 730	cgc Arg	2693
cat His	acg Thr	gca Ala	gtg Val 735	aca Thr	ggc Gly	aca Thr	gcc Ala	aaa Lys 740	agc Ser	ggt Gly	gtg Val	acg Thr	gtc Val 745	aaa Lys	atc Ile	2741
ttg Leu	cga Arg	ggg Gly 750	aag Lys	caa Gln	gta Val	ttg Leu	ggg Gly 755	acg Thr	ggc Gly	acg Thr	gcc Ala	gga Gly 760	aaa Lys	tca Ser	ggc Gly	2789

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gcg ttt tca gtg aaa att ccg gcc cag aag gcg ggg caa gtt ctt cat Ala Phe Ser Val Lys Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His 765 770 775	2837
gtc gcg gca tcg ggc cat cag gcg gaa acc tcg ctc aga acc gtc gtg Val Ala Ala Ser Gly His Gln Ala Glu Thr Ser Leu Arg Thr Val Val 780 785 790 795	2885
gaa aaa gcg ccg aaa aac ccg tcc gtc aaa cgc atc acg aac aaa gat Glu Lys Ala Pro Lys Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp 800 805 810	2933
act gcc gta acg ggt aga acg gca gcc ggc tac acg atc aaa gtg aaa Thr Ala Val Thr Gly Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys 815 820 825	2981
aac gcg tgc aaa aaa gtg atc gcg caa ggc aga gcg gat gca tcc gtg Asn Ala Cys Lys Lys Val Ile Ala Gln Gly Arg Ala Asp Ala Ser Val 830 835 840	3029
agc gtt aaa gtg aaa atc aac aag caa aaa gaa tat gcc gtt ttg tat Ser Val Lys Val Lys Ile Asn Lys Gln Lys Glu Tyr Ala Val Leu Tyr 845 850 855	3077
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acg gtg gct gac gtc atc ccg cca ggc gcc ccg aaa gtt tat cag gtt Thr Val Ala Asp Val Ile Pro Pro Gly Ala Pro Lys Val Tyr Gln Val 880 885 890	3173
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gga aaa ggt gaa tac aag ctg aaa atc agc agg caa aaa gcc gga acc Gly Lys Gly Glu Tyr Lys Leu Lys Ile Ser Arg Gln Lys Ala Gly Thr 925 930 935	3317
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aca gcc gtc act gtg ctt gac aaa acc ccg ccg tct gcg ccg aag gtg Thr Ala Val Thr Val Leu Asp Lys Thr Pro Pro Ser Ala Pro Lys Val 960 965 970	3413
aat ccg gtg aca aac aag agc acg gcc gtt aag ggg aaa gca gaa gcg Asn Pro Val Thr Asn Lys Ser Thr Ala Val Lys Gly Lys Ala Glu Ala 975 980 985	3461
aac gcc gcc atc atc gtc aaa tca gga aag aaa acg atc gga acc ggc Asn Ala Ala Ile Ile Val Lys Ser Gly Lys Lys Thr Ile Gly Thr Gly 990 995 1000	3509
aag gcc gat aaa aaa ggc gcg ttt ttt gtc aaa ata aaa aaa caa Lys Ala Asp Lys Lys Gly Ala Phe Phe Val Lys Ile Lys Lys Gln 1005 1010 1015	3554
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1035 1040 1045

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<211> 1047

<212> PRT

<213> Bacillus licheniformis

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Asp Ser Val Pro Asn Asn Glu Thr Thr Leu Thr Ser Ala Ser Pro Val
35 40 45

Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His Trp Tyr Lys Val Asn
50 55 60

Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His Phe Arg Val Lys Leu
65 70 75 80

Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr Ser Ser Leu Glu Asn
85 90 95

Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn Gly Tyr Ser Tyr Glu
100 105 110

Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala Trp Lys Gly Pro Tyr
115 120 125

Tyr Ile Lys Val Glu Asn His His Asp Glu Glu Asn Glu Thr Thr Ser
130 135 140

Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu Gly Val Thr Leu Pro
 145 150 155 160
 Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro Ala Glu Leu Ser Val
 165 170 175
 Ser Glu Arg Glu Thr Gly Lys Gly Ile Leu Lys Gln Leu Arg Thr Ile
 180 185 190
 Arg Asp Glu Val Leu Ser Lys Thr Glu Lys Gly Lys Glu Leu Ser Ser
 195 200 205
 Leu Tyr Tyr Lys Ala Ala Pro Phe Ile Ser Ala Lys Met Leu Phe Asn
 210 215 220
 Lys Ser Met Arg Asp Ser Val Tyr Lys Asp Leu Val Gln Leu Lys Pro
 225 230 235 240
 Leu Phe Ala Asp Val Ala Lys Asn Gly Gln Val Ser Ala Tyr Ser Ile
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 Thr Asn Asp Asp Gln Lys Ala Ile Ser Arg Leu Tyr Glu Thr Ala Arg
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 Ala Ser Val Pro Glu Pro Leu Lys Lys Gln Leu Asp Gln Val Ala Lys
 275 280 285
 Asp Ile Gly Ile Glu Gln Leu Thr Gly Ser Lys Val Ser Ala Val Leu
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 Glu Lys Ala Gly Met Ala Thr Ala Ser Ser Ser Ala Pro Glu Asn Arg
 305 310 315 320
 Tyr Ile Val Lys Leu Lys Glu Gly Lys Lys Pro Gly Ser Phe Lys Ser
 325 330 335
 Lys Ala Gln Ser Ser Gly Val Gln Ala Leu Glu Pro Leu Gly Lys Ser
 340 345 350
 Lys Thr Ala Phe Lys Asp Met Tyr Val Val Glu Met Lys Glu Ser Arg
 355 360 365
 Ser Ser Gly Phe Lys Ala Ala Ala Lys Gln Tyr Gln Ala Ala Ala Ser
 370 375 380
 Lys Ile Ala Lys Met Pro Glu Val Glu Phe Val Glu Gln Val Gln Gln
 385 390 395 400
 Tyr Glu Ala Leu Ser Arg Asp Thr Gln Tyr Pro Tyr Gln Trp Ser Leu
 405 410 415

Lys Asn Asn Gly Lys Asn Arg Ala Ala Asn Ala Asp Ile Gln Phe Glu
 420 425 430
 Gln Leu Gln Lys Leu Met Lys Gly Lys Lys Leu Lys Asp Thr Val Ile
 435 440 445
 Ala Val Val Asp Thr Gly Val Asp His Thr Leu Ala Asp Leu Ser Gly
 450 455 460
 Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val Gly Arg Thr Ala Asp
 465 470 475 480
 Ala Met Asp Asp Asn Gly His Gly Thr His Val Ser Gly Ile Ile Ala
 485 490 495
 Ala Ala Gln Asp Asn His Phe Ser Met Ala Gly Ile Asn Ala Tyr Ala
 500 505 510
 Lys Ile Leu Pro Val Lys Val Leu Asp Ser Ser Gly Ser Gly Asp Thr
 515 520 525
 Glu Gln Ile Ala Asn Gly Ile Ile Tyr Ala Ala Asp His Gly Ala Lys
 530 535 540
 Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser Arg Val Met Glu Tyr
 545 550 555 560
 Ala Leu Lys Tyr Ala Ala Ser Lys Asn Val Thr Ile Val Ala Ala Thr
 565 570 575
 Gly Asn Asp Gly Val Ser Glu Ile Ser Tyr Pro Ala Ser Ser Lys Tyr
 580 585 590
 Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp Leu Val Ser Asp Tyr
 595 600 605
 Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala Pro Gly Thr Asp Ile
 610 615 620
 Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr Met Ser Gly Thr Ser
 625 630 635 640
 Met Ala Ala Pro His Val Ala Ala Ala Ala Gly Leu Leu Leu Ser Gln
 645 650 655
 Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser Leu Leu Thr Glu Thr
 660 665 670
 Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn Pro Asn Pro Asp Tyr
 675 680 685

Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro Gly Tyr Asp Phe Val
690 695 700

Ser Gly Trp Gly Arg Leu Asn Val Phe His Ala Ala Ser Val Phe Glu
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Leu Asn Met Lys Val His Pro Val Leu Asn Arg His Thr Ala Val Thr
725 730 735

Gly Thr Ala Lys Ser Gly Val Thr Val Lys Ile Leu Arg Gly Lys Gln
740 745 750

Val Leu Gly Thr Gly Thr Ala Gly Lys Ser Gly Ala Phe Ser Val Lys
755 760 765

Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His Val Ala Ala Ser Gly
770 775 780

His Gln Ala Glu Thr Ser Leu Arg Thr Val Val Glu Lys Ala Pro Lys
785 790 795 800

Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp Thr Ala Val Thr Gly
805 810 815

Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys Asn Ala Cys Lys Lys
820 825 830

Val Ile Ala Gln Gly Arg Ala Asp Ala Ser Val Ser Val Lys Val Lys
835 840 845

Ile Asn Lys Gln Lys Glu Tyr Ala Val Leu Tyr Val Ser Ala Ser Ala
850 855 860

Asp Asp His Arg Glu Ser Gly Asp Val Lys Met Thr Val Ala Asp Val
865 870 875 880

Ile Pro Pro Gly Ala Pro Lys Val Tyr Gln Val Ser Asp Lys Ser Thr
885 890 895

Val Ile Gln Gly Lys Thr Glu Ala Asn Ala Gln Val Ser Ala Lys Ala
900 905 910

Lys Gly Lys Thr Ile Ala Ser Gly Lys Ala Asn Gly Lys Gly Glu Tyr
915 920 925

Lys Leu Lys Ile Ser Arg Gln Lys Ala Gly Thr Val Ile Gly Val Thr
930 935 940

Ala Lys Asp Lys Ala Gly Asn Val Ser Lys Ala Thr Ala Val Thr Val
945 950 955 960

Leu Asp Lys Thr Pro Pro Ser Ala Pro Lys Val Asn Pro Val Thr Asn
 965 970 975

Lys Ser Thr Ala Val Lys Gly Lys Ala Glu Ala Asn Ala Ala Ile Ile
 980 985 990

Val Lys Ser Gly Lys Lys Thr Ile Gly Thr Gly Lys Ala Asp Lys Lys
 995 1000 1005

Gly Ala Phe Phe Val Lys Ile Lys Lys Gln Lys Ala Asn Thr Val
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32

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